



STRUCTURE OF EVERNINOMICIN (ZIRACIN)

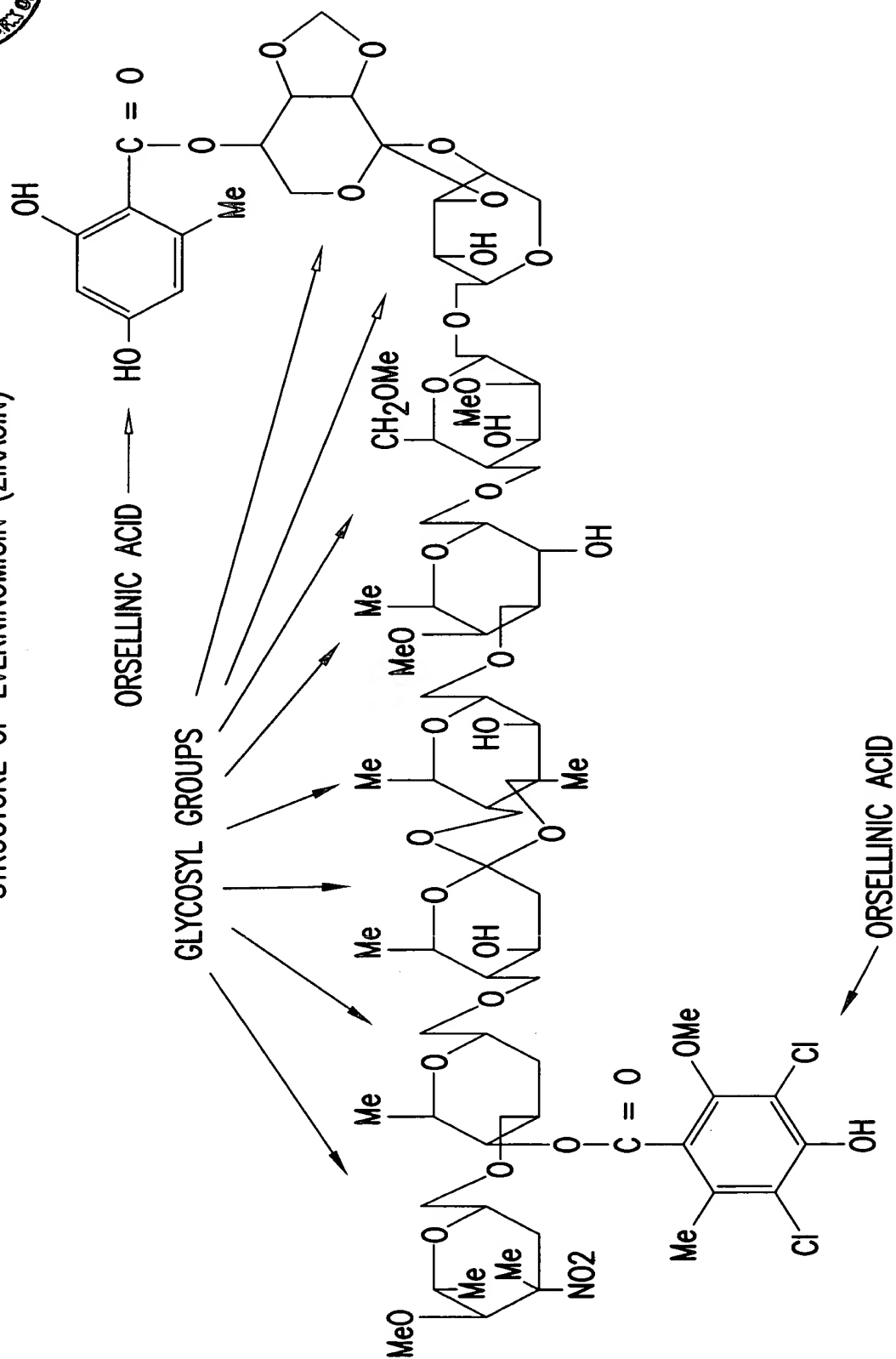


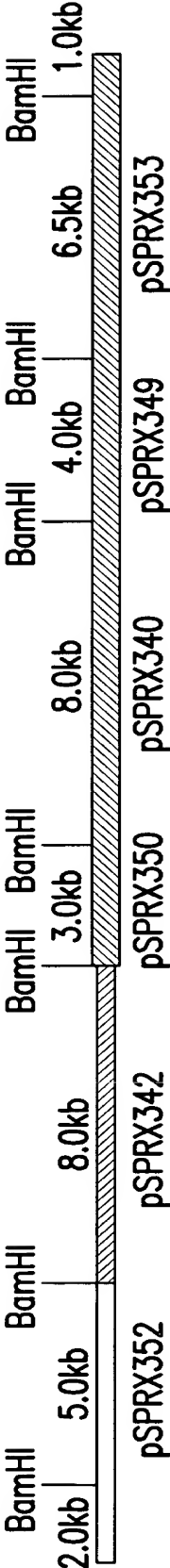
FIG. 1

pSPRX272
37.5kb

COSMID pSPRX272

REGIONS SEQUENCED INDICATED
BY CROSSHATCHES.

FRAGMENTS CLONED INDICATED
BY CLONE DESIGNATION BENIGTH
FRAGMENT.



pSPRX272
(37500 bp)

FIG. 2B

COSMID
pSPRX256

**FRAGMENTS CLONED INDICATED
BY CLONE DESIGNATION BENIGNH
FRAGMENT.**



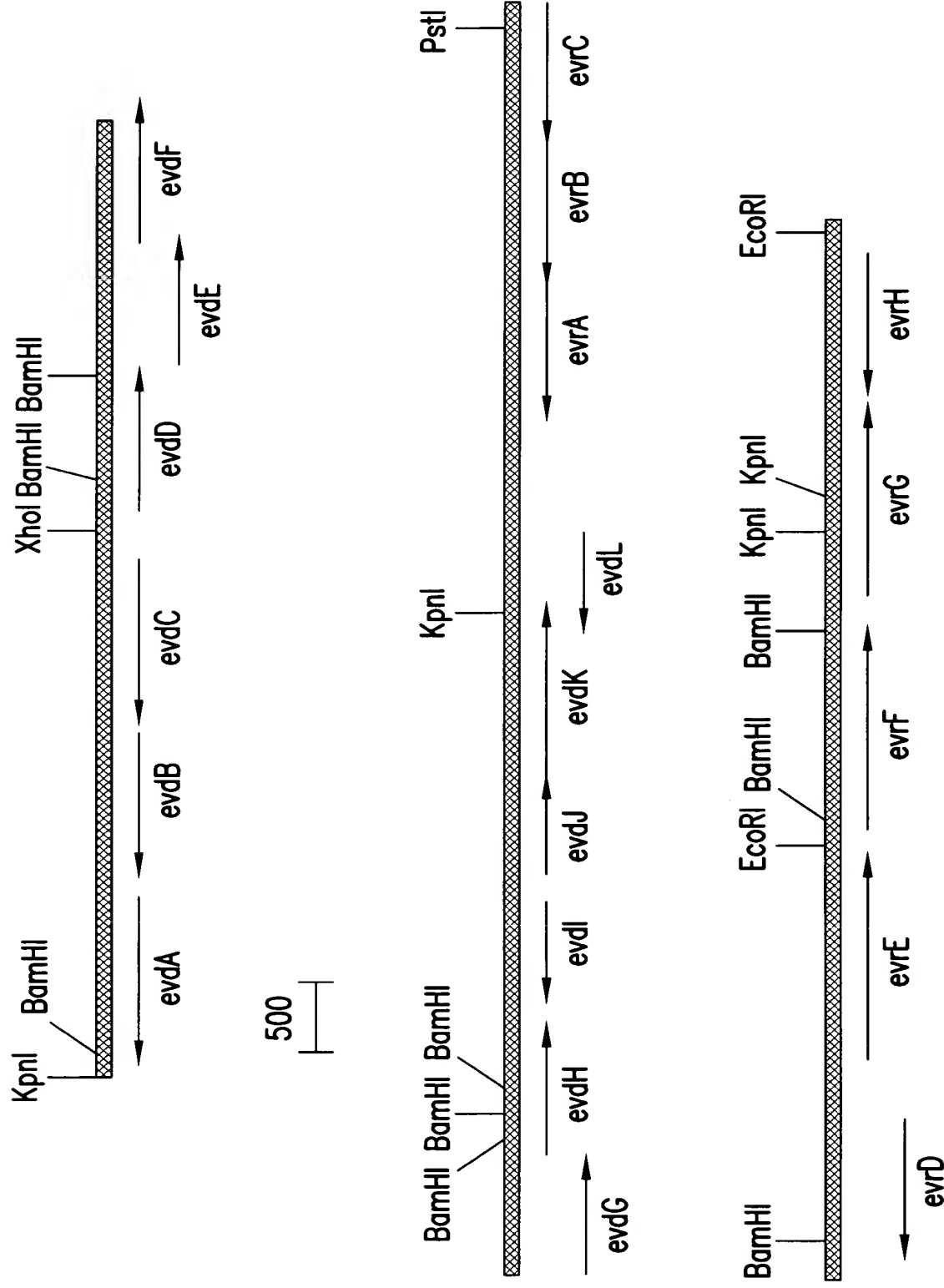


FIG.3A

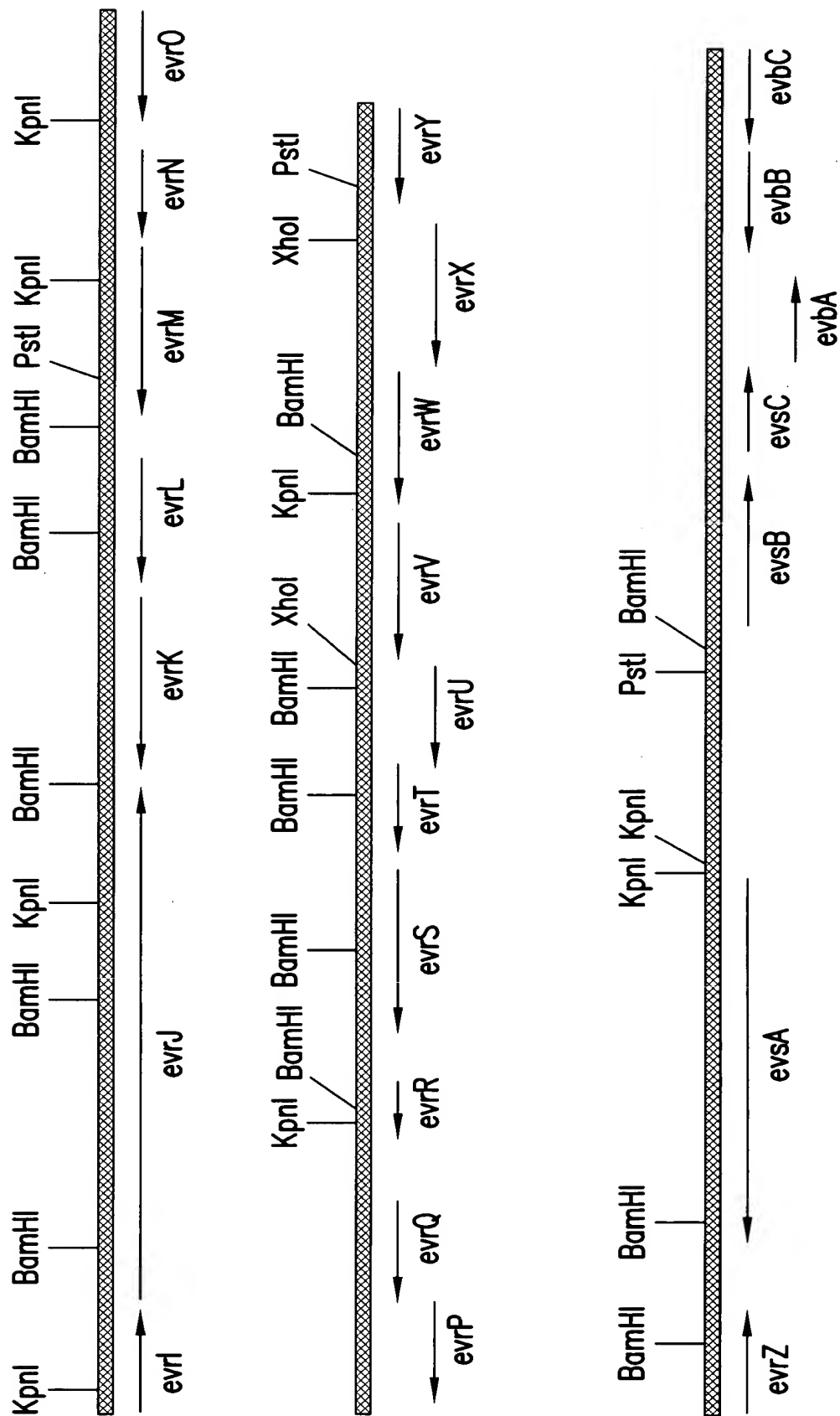


FIG.3B

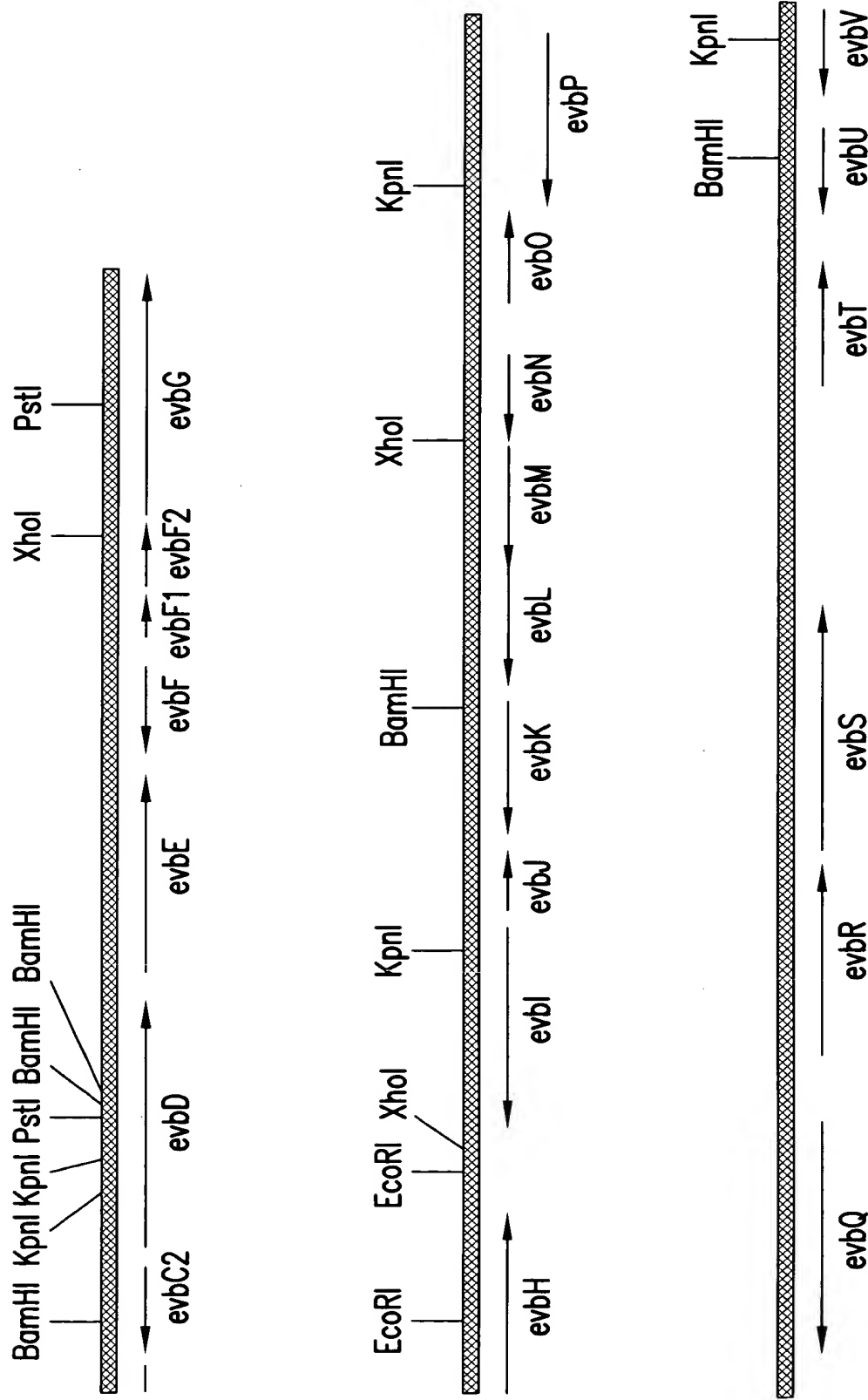


FIG.3C

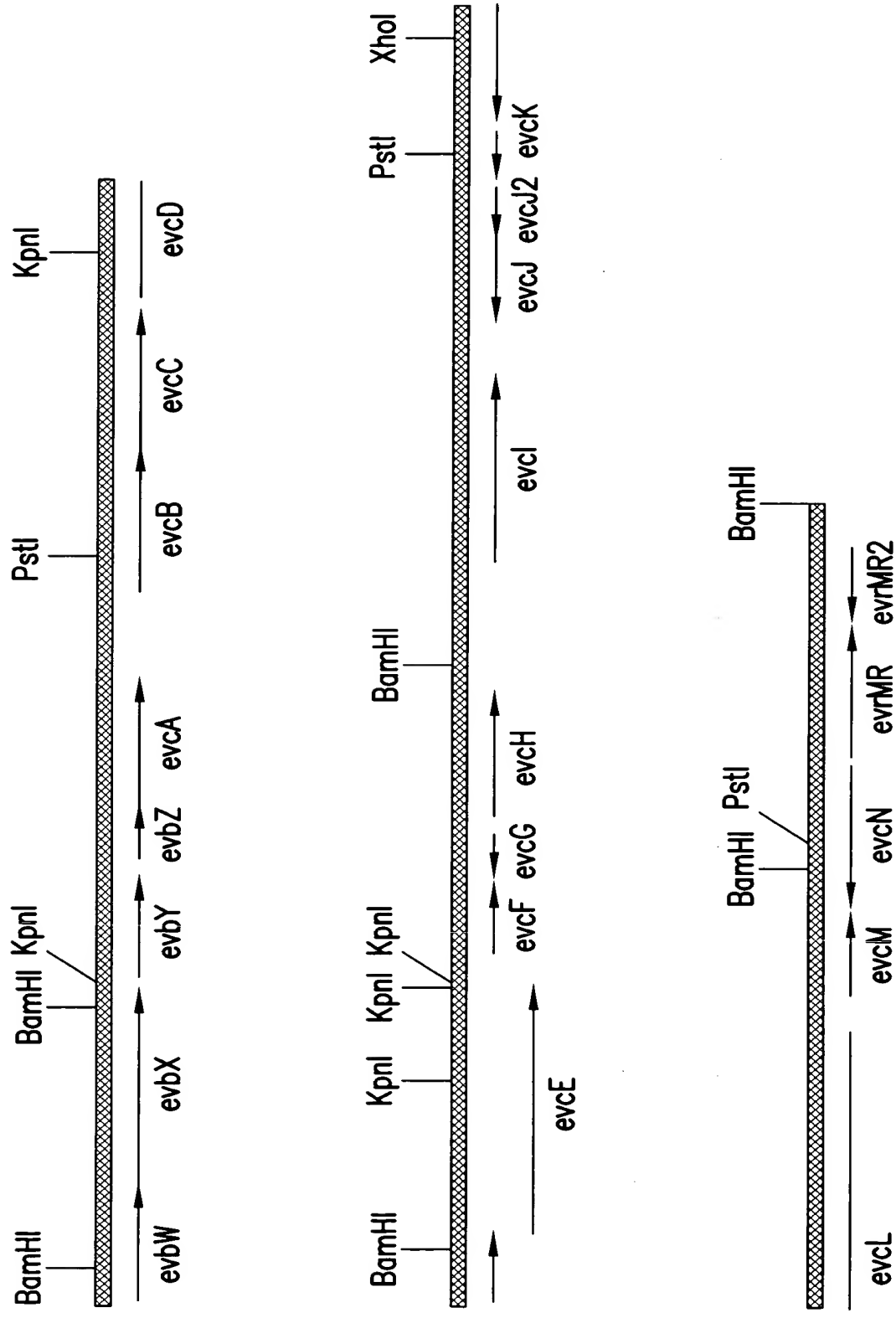


FIG.3D

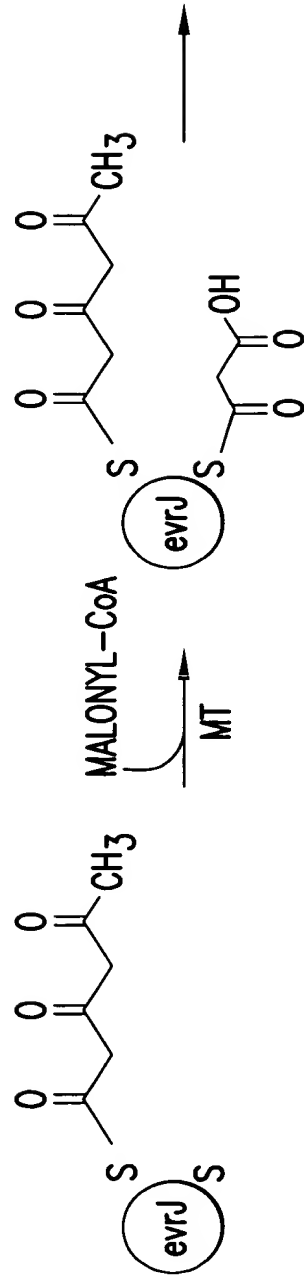
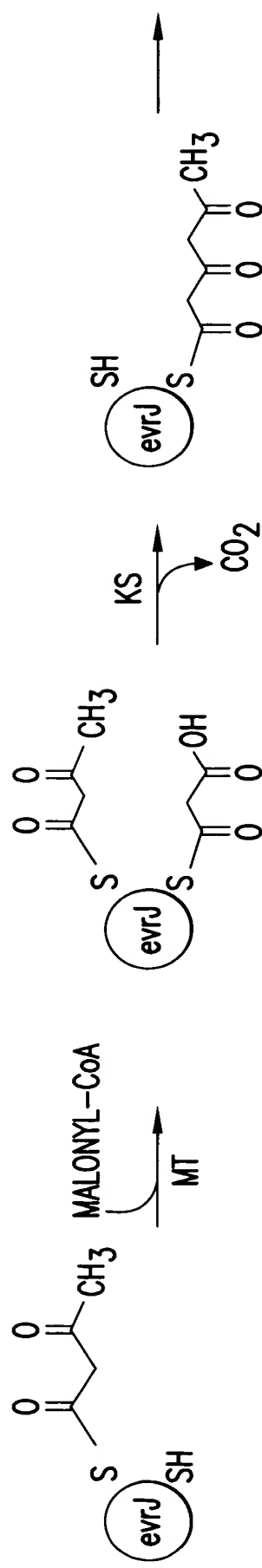
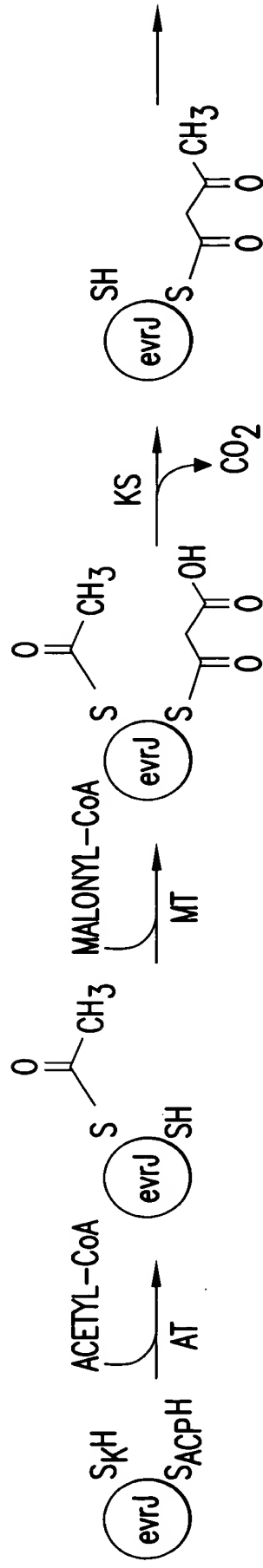


FIG.4A

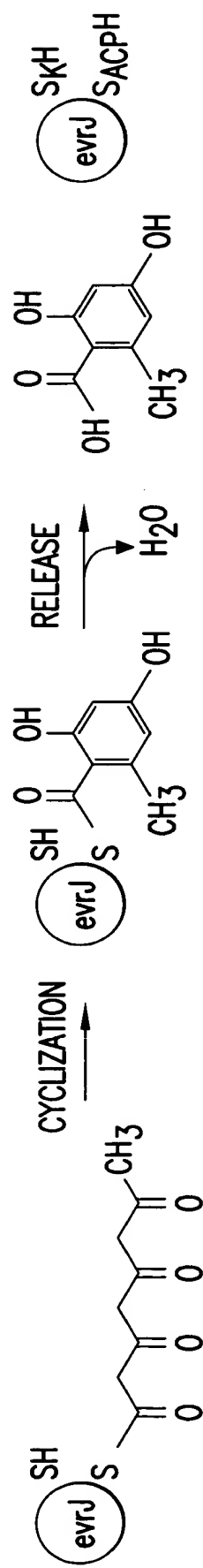
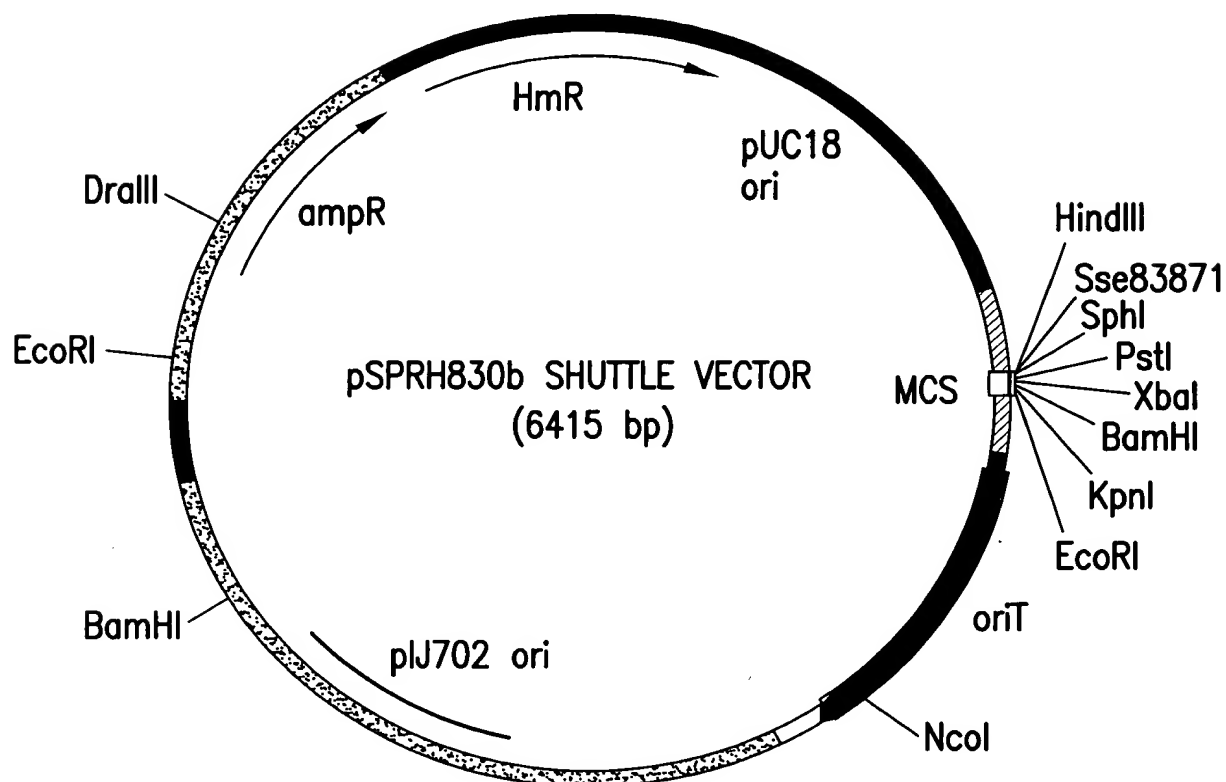


FIG. 4B

pSPRH830b *E.coli*-MICROMONOSPORA SHUTTLE VECTOR

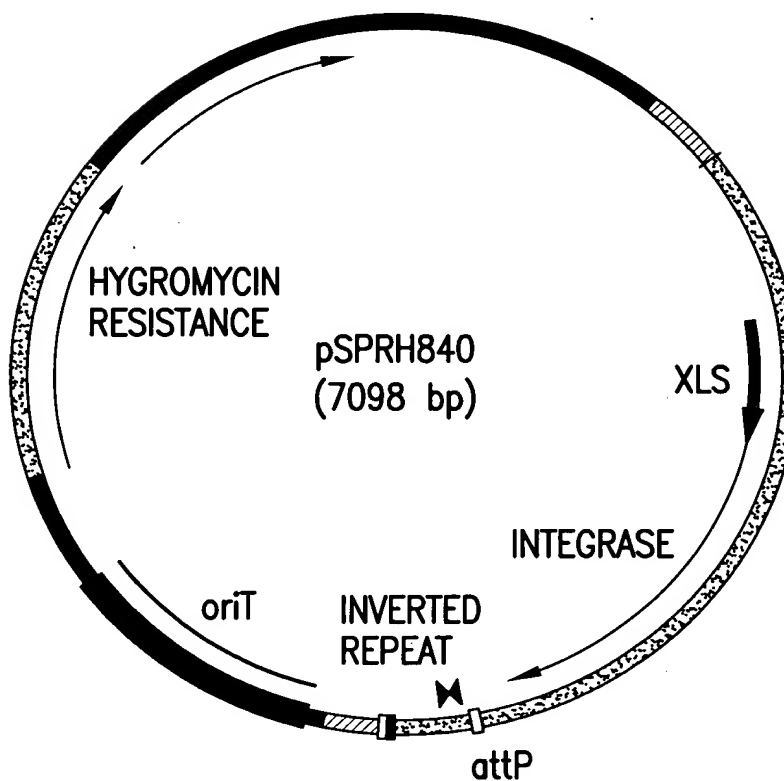


pSPRH830b – pSPRH826b BACKBONE

FUNCTION	SOURCE
– AMPICILLIN RESISTANCE	(pUC18)
– MULTIPLE CLONING SITE	(pUC18)
– pUC18 ORIGIN	(pUC18)
– HYGROMYCIN RESISTANCE	(p16R1)
oriT (ORIGIN OF TRANSFER)	(pRL1058)
pIJ702 ORIGIN OF REPLICATION	(pIJ702)

FIG.6

pSPRH840 INTEGRATING VECTOR



pSPRH840 – pSPRH826b BACKBONE, pMLP1 *xis*, *int* attP INSERT

pSPRH840 CONJUGATED
FROM *E.coli* INTO

HmR TRANSFORMANTS OBTAINED

M.CARBONACEA

+

M.ROSARIA

-

M.HALOPHITICA

+

FIG.7A

1 GTACCTGGCCTTGATCGTGGGGTGGCCGGCTCGGCCGGCT????TCGTGTCGGGTAGGGTCTGGGACATCTGGACTCCTTGCTTGGGTAGGC????CGGGTGGGAGCCTC
117 GGC CGGTGGTGGGGCTCGTCTGGCTCAGGCCCGCAGCAGCCCGGGCTGGTCCCGCCGGGGCTTGGGCTTGATCGGTCGGCCGGGGGCTTCGGCGGCCCTCGGGCGGGTTG
233 GTGGGGCGCGAGGGGAGAGCTCGGCTTTTTCGGCCCGAAGATGCCAGCAGGGGGCGCGTGGGTGGCTCTCTTGCTCTCAAGCCAGCGAGCATGTCTGCTCTCGTCGAA
349 GCGGGCGTCCCGCCGACCCAGGTGATCGGCAGGGTCCGGCGGTGATGGGTGGGAACCCAGGTACCTCGAGCCGAGCGGGGGGAGCTGCTCCTTGTTTCATCAGCGGCT
465 TCATGCGGGCGCTCGAACAGGTCTCGACCTTGGTGCAGGGGTGGGCCATGTGAGGGCAGCTCAAGGCTGGGGTCTGCCCTTGCGGATGGCGAGCAGATTGACCCGAT
581 CCATGCCGCACAGTGGCGCCCGAGCGGCGTTGGTGTGGCGCCAGCTTCGGCGGGGAGGGGTGCAAGACGTCAGTGGTAGCCGAATCCGGGATGGGACACGTATGCCGCGATTG
697 ATCTCGGGAGGTGCTGCACTCATGTGCAAGCTAGGGTGTGCACTGTGTGCGACCCCTCGTACTTTCGGCCGATTCAGACCGGCCCTCCAGGACCCCTACTGTTGCATCAGTGCA
813 ACACCTATGAAGGGAAGCAAGATGCCCGGCCAGAGAGGGATGGCGGTAGGCCAAGCGACGATCAAGATGTGGAGCGCAGTGGGTGTTCGGCAAAAGGCAAGCGACAGGTCCGCAACC
929 GGTCCGACCTGCGGTACGACCTACGGTGTGCAC**ATG**CGGCAACACACCGGGGTGGGGCGCGGCACATGGGCCGATACGTCTCACCGCCCGGAGCGCGGCGGACTGACCAAG
1▶ M R N T P G L G R G T W A A Y V L T A R E R A G L T K
1044 AGCGAGTTGGCCAGGCGCATCCAGAAGGACCGGGCCACCGTGGCCGGTGGGAGGACGGCAAGAACCGGCCCGACGACGGCGGACCTCGTTGCCCGCGGTGCCCCAGGTGCTCGGCCT
28▶ S E L A R R I Q K D R A T V G R W E D G K N R P D D A D L V A R V A Q V L G L
1160 CGACCTCGACGAAGCCCTCGCGCGCGCAGGTCTGCGCCCGGGGTCAACCCCGCAGCGACCCCAACCATGGACCTGGACGAGGAATCGAGCTGGTCCGCACCGACCCCAAGCTGG
66▶ D L D E A L A A G L R P G V T P P A T P T M D L D E I E L V R T D P K L
1276 ACGAGGACATGAAGCGCGCATCATGCCCTAATCTGGAGGCCGTGAGCGCGACAAGGCGGGCGGATCGAGGAACCAAGGGCTCATCGACCTGTTCCGCGGAGCT**GA**CA
105▶ D E D M K R R I I A L I L E R R E R D K A A A I E E T K R L I D L F R R S •

FIG. 7B(1)

1391 **ACGGTGTG**TCGAGAAAGCGGGCCCGTCTACCGCATTCGGGACCTCGTTCCGGGTAAAGGTCACCATTCAGACCGGTTATCCGACGAAGACCAGCGCCAAAGATGCGATGG
1► V W I E K N G P V Y R I R D L V R G K K V T I Q T G Y P T K T S A K N A M
1506 TGCAGTTCGGTCCGGAGCAGTTGCAGGGCAACCGGCTCATGCCGCGGGGGGTGAGATTACCTCGCCGATTTCGTGGGGGAGTGGTGGCCGAGCTACGAAAAGACGGCTGAAACCG
38► V Q F R A E Q L Q G N A L M P R G G Q I T L A D F V G E W W P S Y E K T L K P
1622 ACCGCCGTGAACTCGGAGGGCAACCGGATCCGCAACCACCTCTGCCCATACTGGGCCATCTCACCTTTGACGAGCTGGACGGGCAGGTCACCAGCAGTGGGTCAACGACCTGGA
77► T A V N S E G N R I R N H L L P I L G H L T L D E L D G Q V T Q Q W V N D L E
1738 GGCCGGCGTCGGCCCGTCCACGGGGGTGTCGGGAAGCCGTGGCAGCGAAGACGATCAGCAACTGCCACGGCTGCTGCACAGCATCTCGCGCGCGGGCATCGCGG
115► A G V G P W P E S T R G R R K P L A A K T I S N C H G L L H T I C G A A I A
1854 CGAAACGGATCAGGCTCAACCCGTGCTCTTCGACGATGCTGCCCGCGGCGAGCCGAAAGAGATGAAGTTCCTGAGCGACCCGCGAGATCGGTTCGGCTTATCAGCGCGCTTCGCGCG
154► A K R I R L N P C S S T M L P R R E P K E M K F L S D P E I G R L I T A L P P
1970 CACTGGCGACCGCTCGTTCGTGGGACCGGCTCTGAGGTGGGTGAGCGGATCGGCCTGCGCGCGCGCGGGTTCGACCTGCTCGCGCGCGCGGCCCGCGCTGACCGTCGT
193► H W R P L V M L L V A T G L R W G E A I G L R A G R V D L L A A R P R L T V V
2086 CGAGCAGCTCAGGAGCTGGCCAGCACGGGAGAGCTGCTCTCCAGTCGCCGAAGACCGGAAGGGCCGGCAGCGTCAGTTTCACCACGAAAGTCGCTCTACTGCTTACGCCAC
231► E Q L Q E L A S T G E L V F Q S P K T A K G R R T V S F T T K V A L L L T P
2202 TCATCGCCGGAAAGATGACGAGGTGCTGTTACCGCGCGGAAAGCGGGATGGTAAGSACCGCGCAATTCGGCGGATCTGGGTCAAGGGCTGCGAGGAAGCGGGCTTCGG
270► L I A G K K S D E V V F T A P K G G M V R T R N F R R I W V K A C E E A G L P
2318 GGGTTACGCATTACGATCTGGCGGCACACTCAGCGGGCGGATCTGATTCTTCGCGGGCGTCCGCTGTCGGCGGATCTCCGCGCGCTCGGTCACTCGTCGATCGCGGTACCGGATCT
309► G L R I H D L R H T H A A I L I S A G R P L S A I S R R L G H S S I A V T D L

FIG. 7B(2)

2434 GCTGTACGGGCACCTGCGTGAAGAGGTGACAGAGGGGATCCCTCGCGCGGATCGAGGAGGCGATGGCCGGCGTCCGGCTGAGGAGGTGAGGGGAACTCGACGAGGAGCTGACGG
347► L Y G H L R E E V D E G I L A A I E E A M A G V R A E D L E A E L D E E L T

2550 ACGTGTGGCGACGCAGCA**TGA**TCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACACGAGGTCAGGTGGCCCTGT
386► D V L A D A A •

2665 TGACCCCTGACAGGGCCCGGTAG**CGGGTTCAATTCCCATCAGTCACCCG**GCAAGTGGATCTACTCCACAGCAGATCAGGCCCCCTCCGAAGAGGGGGCCTG

2768 ATGGGTCATAGGGACAGGTAGGGGA**CTCA**ACCCCGGCTCCTTGCTCGGTGGGTGATGCCGTCCGGTACCCCTCCGGTACCTGGCCCTCTCCGTTCCCTCGATCTCGGG

2884 GCGAGCTGATCGGCGAGGTGCGGCTCCATCGCCTGCCGGGTTTGGCCGTTCTGGCTCGAGGCCAGGACCCCGGGCCACTCCGACGCCCCCGCGGGGGGCATGGCGGATCCGGG

3000 CCAGGGCGGAAGCCCTCCGTACGGCCCTCCAGCGCAACCGCTCCAGCTCCGTCTGGTGGCCGGCTGGTCCGGCTCGATGTCCGGGGCCATCGACTCGATGACGTCCTGGTAGT

3116 GCTCCCGCTCGTGTGCCACTGTCGGCTCGGGGGGGGCGAGGGCTTGGCAGTGGCAAGCGACGGCGGACGCCGAGCAGCGGGGAGGGTGCAACGATCGATCATCGTGTCTCATC

3232 ATGGGTCCGTCTCCGATCAGCGACCCCGGGGGGGCGTCCAGGGAGGGGTGATCGTTTCGAGATGGATGTACACGGCGTACTCCTCAGTTGGAGACTCGCCTCGATCAGACA

3348 CCCGTTCCACTGGTGACCGAAAGCCCTGCTCGGGGACACTCCAGCACCCAGCGAGCTGGTGGTGGTGGAACTTCCACGTGGTAAGGGTTACTCAGAGTGATGTTTCATAGGG

3464 TGGGGCCCGTCCACAAATGACGTAGAGTGGCCTTACCATGACATTCCGTGATATTGAGCTGTGGCTTACCGGTGGTAACTTCCAGATTGCGGGGCGAACACGGG

3580 AACCCGGATCAGGGCGCGGAATGCCGACGCCCTACCTCATCCGCGGATATACATCCATCAGCCCGTCCGGATTGGGCACCAACACCGGCACACCTCGGGGATGTTTCACTC

3696 CGCTCGCTCCTCCGGCGTGGGCATCCGGGCCATGACGA**ACTGGTCCGGCTCGCC**CACAGCTCGTCCAGTTCGACCGGCCCGCCGACCCCGGTGCCCTCGCCCCCGAGGGCGGCTCGA

FIG. 7B(3)

3812 CGAGTCCCTCAGCGCGCAGCTCGGGGACCGCCCGTGGCACGGTGCCTTGCACACCCGTACTCCTGGCTCAGCCGAGTCTCGCTGGGCAGCAGCCCGCCCGCAGCGTAGGTGCCG
3928 TCCTGGATGCGGGCGGCGCAGCAGCGCGGCCAGCTGGAGGGCGGCGGGCACACCGGAGTGGGGGTGATCACAGGCCGGACGGTAGGGA TGCCGGGGCGGACGTTGCGCCCGGGCGCAA
4044 CGTTCGAACGTTGGTGGCTCTATGCCCTGGGCCACGTATACCCCTGCTCCGGCGGGCCCCACGGTAAGCCCGCGGTCCCGGGTGAGCTCCAGGGCGCGCTGGATGGTCGACACGC
4160 TGACCGAGTACAGATCGGCCAGCTCTCGCAGCGACGGGAGCTTCGACCCGGGCGGGTACTCGCTGCTGCGGATGGGGCGGTCAAGTCTCGGCGATCTGGCGCGACGACATGGGG
4276 ATGGGCATGGCGGATCTCCCTGGTTGGCCGCGGATGACATCAGCCCGCCACGCTGCCTCAAGCAGTGATTGACCAGTAGTCACACAGTGACCTAGGTGGCCGATGGGTAC

FIG. 7B(4)

pSPRH826b INSERTION PLASMID

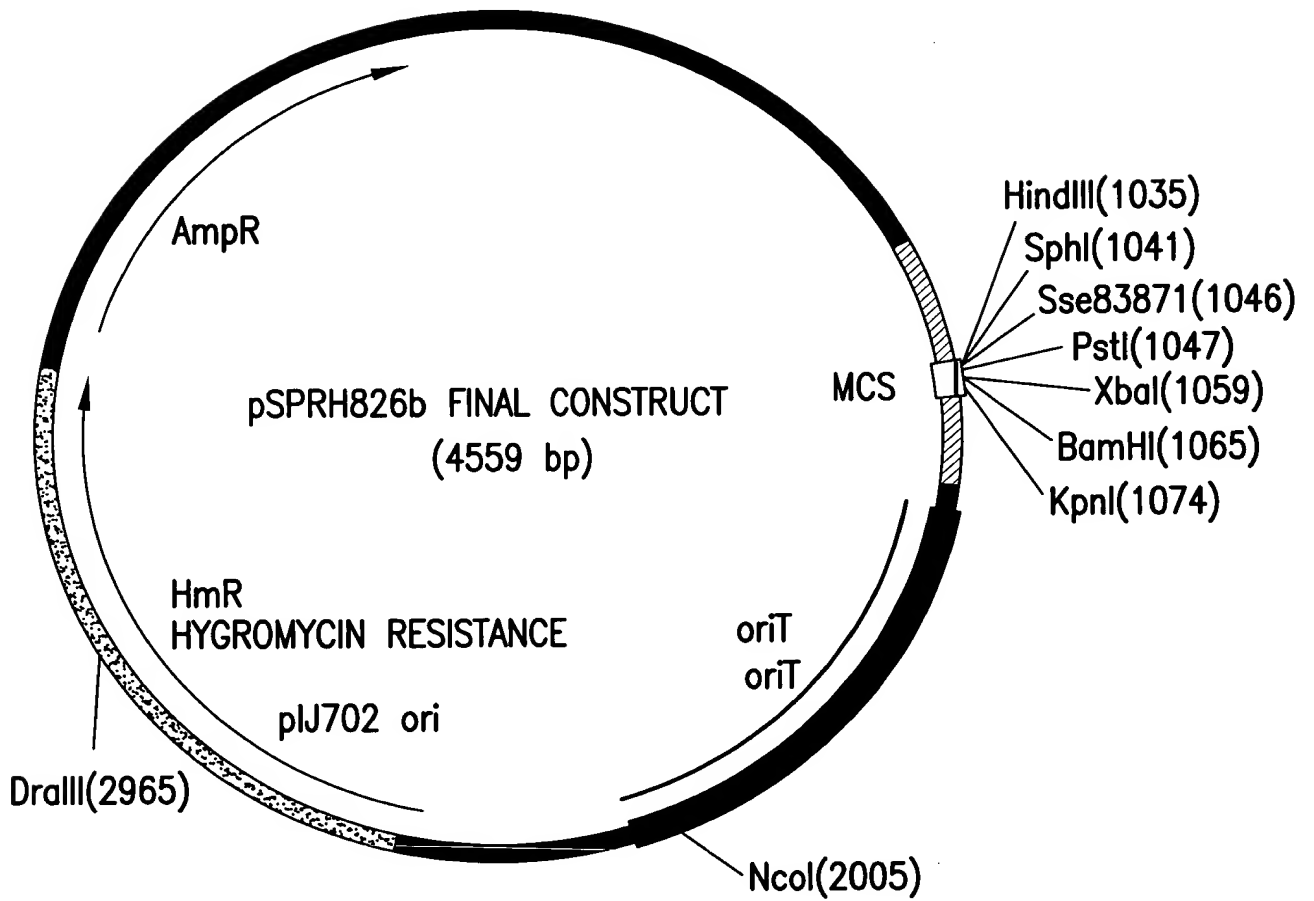


FIG.8

Analysis of *M. Carbonacea* and *M. Halophytica* pSPRH840 insertion site AttB/AttP region

Alignment of pMLP1 attP region with religation clone edge sequence

M. Halophytica PstI relig-9	TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGAGCGCCCGGAGCAATCCGGA	60
M. Carb PstI relig-1	TGATCAACTCTAGGGGAGGGGTAGGGGAAT-CNCTCCGGAGAGCGCCCGGAGCAATCCGGA	59
M. carb PstI relig-4	TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGAGCGCCCGGAGCAATCCGGA	60
pMLP1.intTGA.att region	TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGAGCGCCCGGAGCAATCCGGA	60
Consensus	TGATCAACTCTAGGGGAGGGGTAGGGGAATCCNCTCCGGAGAGCGCCCGGAGCAATCCGGA	60
M. Halophytica PstI relig-9	GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTGACCCCTGACCAGGGCCCCGGTA	120
M. Carb PstI relig-1	GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTGACCCCTGACCAGGGCCCCGGTA	119
M. carb PstI relig-4	GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTGACCCCTGACCAGGGCCCCGGTA	120
pMLP1.intTGA.att region	GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTGACCCCTGACCAGGGCCCCGGTA	120
Consensus	GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTGACCCCTGACCAGGGCCCCGGTA	120

FIG.9A(1)

M. Halophytica PstI relig-9	CGGGTTCAATTCCCATCAGTCACCCAGGTAAGACCCAGGTCAGGGCCGGTTCTCACC-G	179
M. Carb PstI relig-1	CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG	174
M. carb PstI relig-4	CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG	175
pMLP1.intTGA.att region	CGGGTTCAATTCCCATCAGTCACCC---G--GCAAGTGGATCTACTCCACAGCAGATCAG	175
Consensus	CGGGTTCAATTCCCATCAGTCACCCAGGTAARSAMSHRGRYCHVSKCRSWKCDABSRG	180
M. Halophytica PstI relig-9	GCCCT-GACGCATTTTCAGGGG-----	200
M. Carb PstI relig-1	GCCTTCGGCGT-TCCTGAGGGTTCGCG--	200
M. carb PstI relig-4	GCCTTCGGCGT-TCCTGAGGGTTCGC--	200
pMLP1.intTGA.att region	GCCCCCTCCG-----AAGAGGGGGCCTGAT	200
Consensus	GCCYCKVCGYATYHWSAGGGKCSYGAT	209

FIG.9A(2)

Insertion junction

pMLP1 attP region

1	TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAGCAGGTACGGTGGCCT
94	GTTGACCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCGGAAGTGGATCTACTCCACAGCAGATC
174	AGGCCCCCTCCGAAGAGGGGGCCTGATGCGTTCATAGGGGACAGGTAGGGGAACCTCAA



FIG.9B

CLONING SCHEME TO TEST POTENTIAL RESISTANCE GENES

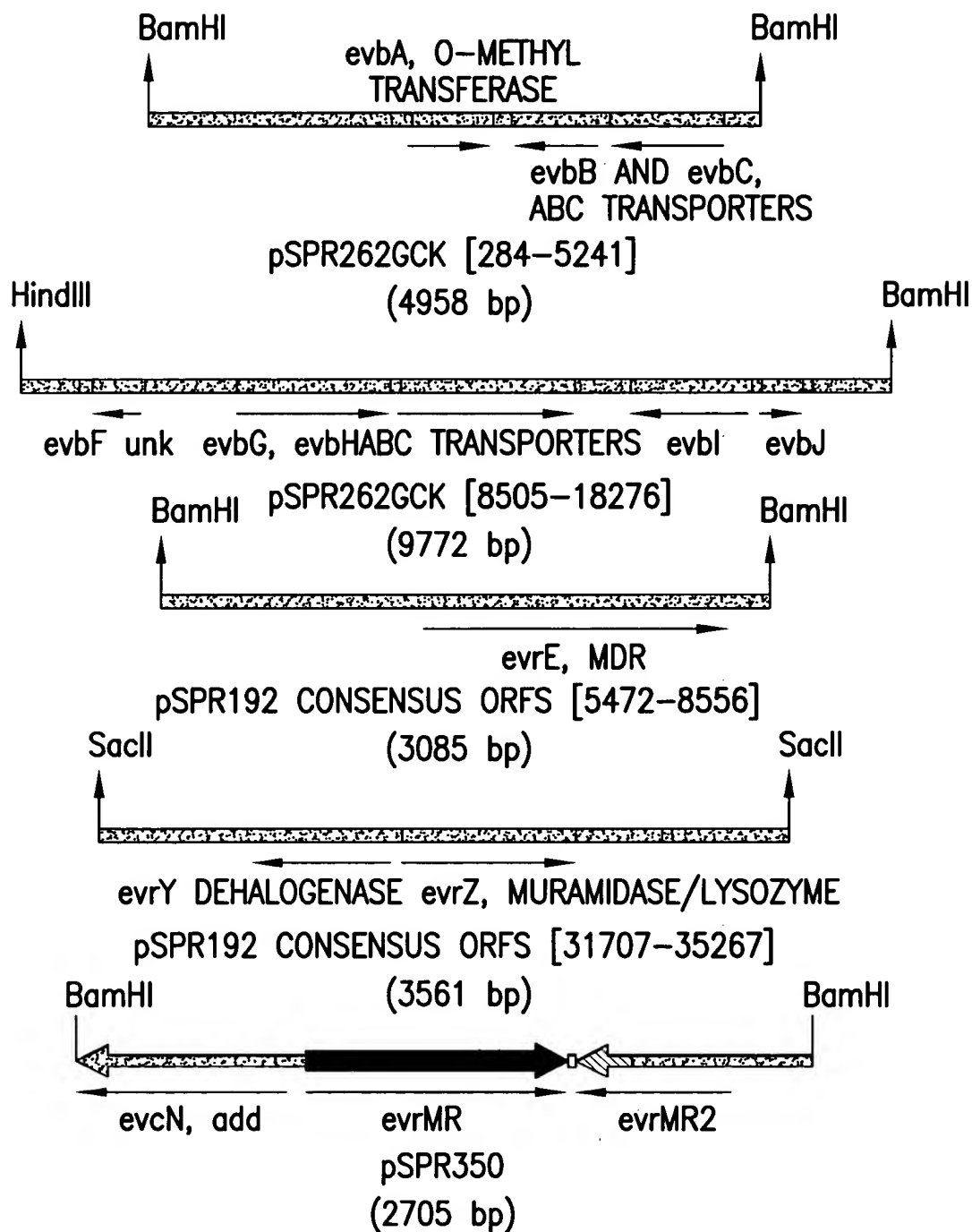


FIG.10

1 GGTACCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGAGAGGAACACCCCGGTAGTCGGGTAGACGGTGGGCGCGAAGGCGGTAC
93 GCGCCTTCGACGGTCAGCGGGCGGGACACCGGGGTACGTCAGTCACGTGTACGCGGGGACGTACAGGATCCACTGTCCGCCAGCC
< . S T V H V R P V Y L I W Q G G A
184 CGGCGGAACCTCTGCTCCTTCGCCATGATCTCGTGGCGTGGTTCCAGGCGAAGACGCGGTAGTCCACCGCTCGGGCGTGAACGCGTC
<R R F E Q E K A M I E D A H N W A F L L A Y D V A D P T F A D
276 CGGGGTGCGCACCGGATGTGCGTCCGGGGGTAGCCGGCCCTGCTTGGCCGGCGTGTGCGACACCCAGGAGACAGGTCCGGACCGA
<P T R V P I H T G P T L R G Q K A P T T D C V W S V L D P G I
368 TGCCGCAGAAGTTCGTACGGTGGCGCTCTTCGCCGTGCGCGCGTACGCCACCACCGCTTGCCTCGGCCCTTGAGCGAGTTCAGCAGGGCG
< G C F N T V T A S K A T A G Y A V V R K G E A K L S N L L A
460 AGCAGGTGCGGTGCGGATGCCCTCGACGTGCGGGCGGAACCTGTGAGCCGGCTGCGGTGCGGACCCCTCGGGCGTCTCTCGCCGATCAG
<L L D T R I G E V D A A F R D L R S R D A V G R A D E E G I L
552 CGCGGCCACCCGCTCGCGCGGTGCGCGCGCGCACGGGCGATGGTGTAGCGGACCTCCCAACCGTGCACCGGAAGCGTTCCACGTCGA
< A A V R E A P Q R A G A R A I T Y R V E G G H V P L R E V D V
664 CGAGCGGAAGCCGAAGCGGGCCGCCAGCGCCTGCACCGACCGCGCGGAGAGAAGAAATGCTCGTCTAGATCTGGTCGAAGGACGTC
< L A F G F R A A L A Q V S R A S F F F H E D Y I Q D F S T
736 TTGTCCAGGATGTCCCGAGGTACGGGTCTCGAAGACGAAGACCCCGTCCGGTGCACGCGGTCAACGCCCCGGAGGATGGAGTCGAG
<K D L I D G L Y P D E F V F V G D P A L L A D V G R L I S D L
828 GTAGGGGATGTGGCAGATGGTGTGGCCGGAAGATCACATCGGGGGGCGTCCGTGACCCGGCGGGCGGTGGACTCCTCGAAGA
<Y P I H C I T N A A F I V D A P G D T E R V R R A T S E E F F
920 ACTCGGTGACCACCCCGTGCACGGGCCACATCGGCCACCCACCGACGGCTCGAAGCCCAGGTGCCGCACTCCCGCCTCGTGG
< E T V V R V G H G R A V D A V G G S P E F G L H R V G A E H
1012 ACGGTACGAGCATCACCCCGTGTGACGCCGATCTCCACCACGAACGGTCCGGGCGGTGGCTCGTGTCCAGCAGGTGCCGCGCGGT
<V T R L M V G D N C G I E V V F P D P G T A E H E L L H R A T

FIG.11A(1)

1104 GTCGGCGAAGTGCTTCTGCATCACGGAGGAGCCCGACGAGTGGTAGCTCTGGTGAACATCTCCTCCGGGGCACCTCCTCCATGA
< D A F H K Q M V S S G S S H Y P Y D Q H F M E E R P V E E M L
1196 GCTGCACCATGTGCAGCCCGCGCAGACCCACCGCCAGGTGGAAGAAGAACTCGTCCGCGAGCTGGTCTCGGTGAGGAACCGGTCGGAG
< Q V M T C G A C V G V A L H F F E D A L Q D E T L F R D S
1288 AGCGGCTGCCGACCCAGGTCGAGGAAC TGGGCGGTGGTGC CGCCACACGCCCGG CAGGTGCCGCGCGGGGCGTGCCGTCGGCTGAATCGGT
< L P Q R G L D L F Q A T T G G C A R C T G R R P T G D A S D T
1380 CATCGCATTCCTTCATGGATACCCCTGCCTCAGGCAGGGCGGATGTCAACGACGTCTCCTTGTCGGGATGGGTGTCAGCTCTCGGC
< M
1469 TGCGGCGTGCCGGCGGCGACTCAGAGCGCGCGAGCACGTGCGCGAGCGCGTGCATCACCCGGTCTCGGTCTCCGGGCGCAGCGAGGGA
< . L A A L V D R L A D I V R D Q T E P L S P
1560 TACATGGGGAGGAGAAGATCTCGCCGGCCAACCGTTCCGTGGTGGGAGGGAGCCGGTCTGGTAGCCGAGCTTGGCGAAGCCGGTCATGGT
< Y M P L S F I E G A L R E T T P L S G T Q Y G L K A F G T M T
1652 GTGCACCGCCAGGGTAGCTGATGTTGAGCGCGATGTCCCGCCGCCCAACTGTTTCAGGATGCGGTGCGGGCGGGGTGGCGGACCCAGCT
< H V P W P Y S I N L A I D R A A L Q E L I R D R A P H R V V Y
1744 AGACGTACCAGACGTGTTGTTGCGGTGCGCGGTACCCGGCAGGGTCAGGCCGACCTGGTCGGCGATGTGGCCAGGCCCTCCTCGTAGCGC
< V Y W V H E N D T A T V P L T L G V Q D A I D A L G E E Y R
1836 CGGGCCACGGCGGGCGCGCGATGTAGTCGTGAGCCGGCACAGCTTGGGGCGCAGGATCTCGGCCTGCACCTCGTCGAGCGGCAGTT
< R A V A R R G A I Y D D L R C L K R R L I E A Q V E D L R C N
1928 GTGCCCCGGCGTCTCGACGACGTAGTACCTGTTCCATGCCGTAGTAGCGCAGCCGCGCAGCGCTCGTCGATCACGGCGTCCGCGGTGA
< H G P T E V V Y Y V Q E M G Y Y R L R R L R E D I V A D A T V
2020 CCACGCCGCCCGCTGCCGTACGGCGCCAGCACCTTCGTGCGATAGAACGAGAAGCAGCGGCTGCCCATCTGTGCCGGCCAGCCGTCGG
< V G G D G Y A G L V K T P Y F S F A A A D G M T G A L R G
2112 CCCCAGCGCGCGGTGCGGACTGCGCGAGTCCCTCCAGGACCTTGAGGCCGTGTTCCGGGGCCACCCGACGACCCGGGTCCATGTCGACGCA
< G R R A G H S Q A C D E L V K L G H E R A V R L V P D M D V C

FIG.11A(2)

2204 CTGGCCGTAGAGGTGCACCGGCAGCAGCCCTTCGTCCGGGGGGTGACCGCCTCGGCCAGCAGCTCGGTGTCCATCAGGTAGTCGTGGCGGC
 < Q G Y L H V P L L A K T R P T V A E A L L E T D M L Y D D A R
 2296 GGACGTCCACGAAGACCGCGTCCGCGCAGCGGTGATGGCGAGCACCGTCGGCGGGCGGTGTTGGAGACGGTGATGACCTCGTCGCGCC
 < V D V F V P T A G V A D I A L V T P A A T N S V T I V E D G
 2388 GGCCCGACGTCGAGCGCCTGGAGTGGAGTTGATGGCGTTGGTGCCGTTGTCCACCGTGACGCAGTCGGGCATGTCGTGATAGCGGGCGAA
 < P G V D L A Q L A L K I A N T G N D V T V C H P M D H Y A A F
 2480 CTCCTGCTCGAAGCCGCGCACGCTCGCGCGAGGATGAGGTTCCCGGACTCGAAGACCGTCTGCACGGCGTCGAGGAGGTGTCGCCGTTCCCT
 < E Q E F G R V S A G L I L N G S E F V T Q V A D L L D D R E K
 2572 TCTCGTACTCCGGCAGGTAGCCCCACACTCGGATGGTTCATCTTCGCCCTTCTACGCCGAGGTCCGGGAGCGGAGCGCGCACGCTCAT
 < E Y E P L Y G W V R I T M < . A S T R S R L A R V S M
 2661 GTAGTCGTTGCCGGTCGAGTCCAAGTGCCTGACCGCTCAGGTAGTCGACGGCGTCCACGTAGCTGTAGGGTGCATGAACCCGCGGGCCC
 < Y D N D R D L G L A Q G S L Y D V A D V Y S Y P Q M F G G A R
 2753 GCACGTCGCGATAGAGCCGGGAGAGTGGGTGCCCGGCCGTGTAGGCGAGGCCGCCGACAGGCTGAGGCAGTCGTCCACCACCGCGGGGGCC
 < V D R Y L R S L P H G A T Y A L G G V L S L C D D V V A P A
 2845 AGCTCGTTGACGGTCATCTTCGCGTACTGGAACGGGGTTCATCATCCGTCGGCCGCGTTCGTCCGGGTGCGCGGACAGGTCGACCGACGCGCG
 < L E N V T M K A Y Q F P T M M R R G R E D P D G S L D V S A A
 2937 GTCGGCGTTGGTCAACGCCGCGCGCGACCGTGGTGCGTAGCGCGGTAGAGCCGGGTGTCCAGCCCGCGCAGCCGCGCGCGCGCGCGCGT
 < D A N T L A A G V T T R L A Y L R T D L G A V L A R A G A R P
 3029 GCTCGCCGCGCGCGCGCGAGAAACCGACCGCATGTCCCGGGCGCGCTGGGCGATGCCGGCGTAGATGCCGAGCATGGTGATCGAGCTG
 < E G G R G A C F G V A I D R A A Q A I G A Y I G L M T I S S
 3121 ACCGTCTGCCCGGCCAGCACGGCGTCCCGCGGGGCCCGACCGGGCGCGCTCCAGCAGCTCGTCGGCCCGGACCGGGCACCGGTCCGAAGAC
 < V T Q G A L V A D R R A G V P G R E L L E D A R V P C R D F V

FIG.11A(3)

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3213 CACCTCCAGCGTCCCCGAGGCACGCATTCCAGCGCGTCCAGTTGTCCAGCACCGTGAGCCCGGGGGCGTCGCGGTGCACGACCGGCACGG
< V E L T G S A R M G L G D W N D L V T L G P A D R H V V P V A
3305 CGAGGAACACGAGCGTGTGTCGCGCGCTGGCGGTGCACGAAGAAGTGGTGCATGGGCGCCATGCTGACGAGCACCTTGGCGGCC
< L F V S G D D R R Q A H V F F H T A I P A M S V L V K R G
3397 GACAGCAGCCAGCGCGCGCGTGGAAATGCAGTCGGTGACCAACGCCGGGGCGTCTTGAGCGCGCGCAGACGGCGGCTCGCCCTC
< S L L W G G A G D S H L E T V V G P A D K L A G C V A A E G E
3489 CGCCATCGCCCGCAGCAGCGCTCCGCCATCGCGGCACCGCGCGTCCGTGCTGCCACTCGTAGGTGAGGGTGAGGCCCGCGGTGAGCT
< A M A R L L R E A M A R V P P T G H Q W E Y T L T L G R S L Q
3581 GCACGTGCCAGGCCAGCGGTGGACGCTCGGCCTCGGCCAGCGCATCAGCGCGTGCACGTCGTACAGCCGGGTCAACCCAGGCCG
< V H W A L A T S A D A E A L R M L A T A V D Y L R T L G L G
3673 CCCAGCTCGGCGGAACGGTGGCGCCCATCAACCCGAGCTTCGCGAACTGCTCGAACGCCTCCACGGGAAGGTGCCGGTGCCGGTG
< G L E A P V T A G M L G L K A F Q E F A E V P F T G T R D R D
3765 GCGGCGCTCCGCACTGATTCGGGATCAGCGCGGCAAGCAGGTGCAACCGTGCGCCCGCGCGTGAGCGCGCGCGGAAGATCCGCGC
< A A E A S I R P I V G A L L D V V T R G A P T L P A R L D A A
3857 CCACCCATCTCCTCGGTCAGATTAGACATCGCCTGCTCCGTTCGGCTGTGCCGAACCTGTCGTATCAGGGTGCGCGCGATCACC
< V
3947 AATTGCTGGCTGATTGTCCACCGACGATGCTCGACAGGGATACCCAGAAATAGGCGGCAACGGCTTGGCGAAACCCCTGTCGTGCGCGGAGT
4039 TCGCCAAGTCTAGTTGGATCACTCGAGCTTCCCCCGCAGAAGCCGTGAACCATGGGCCAGCGGTGACGTGCTATATATTCGGCCGACACG
4131 TCGGAGGACTCGTGAAGATACTGTTTCATCGCAGGACCGACGAAGTCCAGCCTATTCGGCTGGCCCCACTGGCAATCGCCGCCCGGATG
> V K I L F I A G P T K S S L F G L A P L A I A A R M
4221 AGCGGCGACGAGGTGCTGATGGCTTCCACGCGAGGAGTGTACCGGCGACGATGTCGTGGGCTGCCGGCCTTCCCGCTGGCGGCGCTGAC
> S G H E V V M A S T Q E V V P A T M S V G L P A F P L A A L T
4313 CCTCGCGGAGTCATGACCACCGAGCGGGCGGCGATCCGCTGCGCATCCCGGCGGAGGACGCGCCTTCGTCCCCCTTCGTGCGCGGATGT
> L A E L M T T D R A G D P L R I P A E D A A F V P F V G R M

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FIG.11A(4)

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4405 TCGGCCGGCTGGCGGCGATCAGCTGGATCCGCTGGCGGACCTGGTCGGCGGGTGGCGGCCCGACCTGATCGTCGGCGGGCCGACGCTAC
    >F G R L A A I S L D P L R D L V G G W R P D L I V G G P H A Y
4497 GCCGCGCGGATCCTGGCCACCGAACTTGGGGTGCCCTGGTGCGGCACCTGCTACCGGCAACCGGTGGACCGGAGGGCACCCATCCGGG
    >A A P I L A T E L G V P C V R H L L T G N P V D R E G T H P G
4589 GGTGACGAGGAGCTGGGCGGAGCTGGCCGCTGGCCAGGTGCCCGCTTCCACCTGGCCCTGGACATCTTCCGCGCCAGCA
    >V D E E L R P E L A A L G L A Q V P P F H L A L D I F P A S
4681 CCCGGATCGACGACGTCCGCGCGCGCAGCCGGTGGACCGCTGCGCTGGATTCCGACCAACGACGAGCAGCCGGTGGCGCCGTGATGCTC
    >T R I D D V P P A Q P V R P L R W I P T N Q Q P V A P W M L
4773 TCGCGCGGCGCGTCCGCTGCTGGTACCGCGCGCAGTCTGGTCACCAACCAACCACTTCGACTTCTCCACGGACTGGCGGCGAC
    >S R G P R R V L V T A G S L V T T T H N F D F L H G L A G T
4865 CCTGGCCGAGCAGGACGTGAGGTCTGGTCGGCGCGCGGAGGTGGTGGCGCCCTGCACGACGTGCCGGGTGTGCGGCACGCCGGCT
    >L A E Q D V E V V A A P P E V G R A L H D V P G V R H A G
4957 GGTCCCGCTGGACGTGGTGTGCCCCACTGTGACCTGATCGTGCACCACTCCGGCAGCATGACCGCGTGACCGCCTTGAACGCGGGGGTG
    >W L P L D V V L P H C D L I V H S G T M T A L T A L N A G V
5049 CCCCAGTGTGTCGCGCAGGAGAGCCGGTTTCATCGAGTGGCGGCGCAACCTGTGACCCCTGGGCGTGGCGCAGACCCCTCGCGCCGGGCGGA
    >P Q L I V P Q E S R F I E W A R N L S T L G V A Q T L A P G E
5141 GGACACGCGGAGGCGGTGGGCAAGGTGCCCCGCTGCTGCTGGAGGATCCGGTCCACGCCACCAAGCCGCGCGGATCGCCCGGGAGATCG
    >D T P E A V G K V A R L L L E D P V H A T S A A I A R E I
5233 CCGAGATGCCCGGCCACGGAGGTGTTGGGCCAGCTCACCAGTTCGCGACCCGGGGCCTGACATGCGCGTCTCTGTGACCGCGGAGGCC
    >A E M P G P T E V V G Q L T E F A T R G L T C A S S .
                                     >V T G G A
5324 GGGTTTCATCGGCTCCACCTCACCGACGCGTGTCTGAACGGCGGACAGCGTCACCGTGTCTGACGACCTGTCCACCGGGCGGCCGAGCC
    >G F I G S H L T D A L L E R G D S V T V L D D L S T G R P E R
5416 GCTGCCCCGGGGTGCCGTGCACACGGGTGATCACCGACCGGGCGGGTTGACCCGGTGGCCGAGCAGTGTGCCCCGAGGTCAITCT
    >L P A G V P L H H G S I T D R A G L T R L A E Q C R P E V I

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FIG.11A(5)

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5508 GCCACCTGGCCGCCAGGGCGGACGTGGCGCAACTCGGTGGCCGACGCCACCTCGGACACCGGGGTCAACGTGGTCGGCACCGTCAACGTCCTG
    >C H L A A Q A D V R N S V A D A T S D T G V N V V G T V N V L
5600 GAGGCCGCCCGGGCCATCGACGCCCGGGTGGTCTTCGCCTCCAGCGCGGCGCCCTCTACGGGGAGGTCGACGAGCTGCCCTCCCCCGAGGA
    >E A A R A I D A R V V F A S S G G A L Y G E V D E L P S P E D
5692 CGTCGGCCGGCGCGTGGCGCGCGTACGGGCGCGCAAGTACTGCGGGAGCAGTACCTGGCGCTCTACAACGGGCTCTACGGCTCGACCC
    > V R P A P W A P Y G A A K Y C A E Q Y L A L Y N R L Y G S T
5784 ACGCGCGCTGCGGCTCGGCAACGTGTACGGGCGACGCCAGGACCCGACCGCGGAGCGGGTGTCTCGATCTTCTGCGGCTGCCTGGTG
    >H A A L R L G N V Y G P R Q D P T G E A G V V S I F C G C L V
5876 GCCGGCGCGCGGCGACGGTGTTCGGCGACGGCGAGCAGACCCGGGACTACATCTACGTGGCCGACGTGGTGGAGGCGTTCCTGCTCGCGGT
    >A G R R P T V F G D G E Q T R D Y I Y V A D V V E A F L L A V
5968 CGGGCACGGTGGCCCCGCGCTGTGGAACATCCGCACCGGGACCTCCACCAGCATCCGCAAACTACTGGACCTGGTCGGCCGACCGCGGGC
    > G H G G P G L W N I G T G T S T S I R K L L D L V G R T A G
6060 GCGTCCGGACCCCGCTTCGAGCCACCCCGCTGGGCGAGCTGAAGCACTCCGCGCTGGAGGTGACCCGCGCGCGGGAGCTGCGCTGG
    >R V P D P R F E P P R L G E L K H S A L E V T R A A R E L R W
6152 GCGGCCCGAAGGCTCGCCGACGGCATCGCGAAGTCTACAAGTGGTTCGAGGGGACGAACCGGTCCGGGGGAGCGATGACCCGCG
    >M T R
    >A A R T R L A D G I A K V Y K W V E A D E P V R G E R .
6242 AGGGGTCAACGCCCGGGTTAGGGTCGCCACCATCACGGTCGGCACCAACGAGATCCGTTGGCTGGACCGCGGCTCGGCTCGCTCGGCC
    >E G S T P P V R V A T I T V G T N E I R W L D R A L G S L L A
6334 AGCGACACGCGGCTTCGAGCTGACGGTCTTCTACGTGGACAACGCCCTCGGCCGACGGCAGCGTGGCGCACGTATGTGCGGCTTCCCGG
    >S D T T G F E L T V F Y V D N A S A D G S V A H V M S A F P G
6426 CGTCCGGGTATCCGAAACCCCGCAATCTCGGCTTACCGGCGCGGAACAACGTGCGCATCGGGCGGGCCCTGGCGGAGGGCTTCGACCACA
    > V R V I R N P R N L G F T T G A N N V G M R A A L A R G F D H
6518 TCTTCTGGTCAACCCGGACACCTGGACACCGCGGGGCTGGTCCGCGGGCTGGTTCGAGTTCGCGCAGCGGTGGCCGAGTACGGCGTCATC
    >I F L V N P D T W T P P G L V R G L V E F A Q R W P Q Y G V I

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FIG.11A(6)

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6610 GGCCCGTTGCAGTACCGCTACGACCCGGCGTCGACCGAGTTGACCGACTTCAACGACTGGACGCAGGTGCGCCCTCTACCTGGGCGGAGCAGCA
> G P L Q Y R Y D P A S T E L T D F N D W T Q V A L Y L G E Q H
6702 CACCTTCGCCGGCGACCTGCTGGATCATCCCTCGCACGTACCGCGACGGTCCGCGACCGCGCGCCGCGCACCCCTGGAGCACGGGTACGTGC
> T F A G D L L D H P S H V T A T V R D R A P R T L E H A Y V
6794 AGGGCTCGGCGCTGTTGTCGGGGCGCGGTGCTACGCGAGGTGGCCTGCTCGACGAGGTGTTCCACACCTACTACGAGGAGGTGCGACCTG
> Q G S A L F V R A A V L R E V G L L D E V F H T Y Y E E V D L
6886 TGCCGGCGGGCCGGTGGCGGGCTGGCGGTGGCGCTCCTACTCGACCTCGGCATCCAGCACAAAGCGGCGGTGGCACCCGCGGAGCGC
> C R R A R W A G W R V A L L L D L G I Q H K G G G T A A S A
6978 GTACAGCCGATACACATGCGCCGAACCGCTACTACTATCTGCTGACCGATGTGGACTGGCCCCCGCCAAAGCCCGCCGGCTCGCCGCC
> Y S R I H M R R N R Y Y L L T D V D W P A K A A R L A A
7070 GCTGGCTGTTCTCCGACGTCCGTGGCGGGGGTGGAGGTGGACGCGCGGGCGTGGGGCGCGGAGACCTTCGTGGCGCTCGGGTGG
> R W L F S D V R G R G V T G R T S A G V G A R E T F V A L G W
7162 CTGGCCCGCCAGGCCCGGTGATCCGGGAACGTGTCGGCGGCACCGGCTGCTGCGGGCAGGAGGACGGGCGTGGACCGCCCGCCGAGAGCG
> L A R Q A P V I R E R R R R H R L L R A R G T G V D R A R E R
7254 GAAGGAAACCGTGGGGGATGAGCAGGCCACGGATTCTCGTCGGGGCAACTTCCACTGGCAGGCGGGTTCAGCCAGACCGTCGCCGCGGT
> K E T V R G .
> M S R P R I L V A G N F H W Q A G F S Q T V A A
7345 ACGTGGGGGGCCCGGAGGCCGACTGCGAGGTGGGCTCTGCGGCCCGCTGTCCCGGGTCGACGCCGAGACGGCCCCGGCACCTGCGCGGTC
> Y V R A A R E A D C E V R L C G P L S R V D A E T A R H L P V
7437 GAGCCGGACCTCCGCTGGGGCACCCACCTGGTGATCATGTTGAGGCCAAGCAGTTCTCACCAGGGCGCAACTGGACCTCGTCGAGGCGTT
> E P D L R W G T H L V I M F E A K Q F L T E A Q L D L V E A F
7529 CCCCCGACAGCGCGGCCCATGTCGACTTCGACGGGCACTGGGTGCCGAGGAGGGGGGACGGCGACAGCGCGTCGGGCGGGTACTCCG
> P R Q R R A I V D F D G H W G A E E G G D S A S G R Y S
7621 CGGAGAGTTGGCGGGGTTGTACTCGACCTGAGCGACCTGATCTCTGAACCCCGGCTGGGTCCGCTCCCGCGCGCGCCGGTCTTCAAG
> A E S W R R L Y S T L S D L I L Q P R L G P L P A G A R F F K

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FIG.11A(7)

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7713 TGCTTCGGCCTGGCAGCGCCGGTGCGGCACCCGCTGGAACTGGGCACCGCGCGCAGTCGCGCCCGTACGACCTCCAGTACATCGGCAGCAA
> C F G L A A P V R H P L E L G T G A Q S R P Y D L Q Y I G S N
7805 CTGGTGGCGGTGGGAGCCGATGACCGAGATGGTCGAGGCGGGCGGGCGCCGCGCTGCGCCGGCTGCGGGTGTGCGGACGCTGGT
> W W R W E P M T E M V E A A A A R P L R R L R V C G R W
7897 GGGACGGCGCAGTTGCGGGGCTTCGAGGAGCGACGCTCAGCGAGCGGGCTGGCTGCGGGCGCGCGGCTCGAGGTGCATCGGCCCGTG
> W D G G S C A G F E E A T L S E P G W L R A R G V E V H P P V
7989 CCGTTCGGCCACGTGGTCGAGCAGATGGGCCGGTGGCTGATCTACCGGTCCTGGTGGCGCGCTGGTCACGACACCGGCCTGTTGACCCC
> P F G H V V E Q M G R S L I S P V L V R P L V T S T G L L T P
8081 CCGGATGTTGAGACGCTGGCCTCGGGCAGCTGCCCGTGCTCCCGGTGCGCGGAAGTTCTCGCGCCGGTCTACGGCGACGAGCGGAAC
> R M F E T L A S G S L P V L P V A A K F L A P V Y G D E A E
8173 ACCTGATGCTCGGCGACGACCCGGCGGAACGCTGAGCGGGCTCTCGGCCGAGCACGAACGTCGGACGACTGGTCGGTGAGATTCAGGAC
> H L M L G D D P A G T L S R L S A E H E R Y G R L V G E I Q D
8265 CGGCTCCGCGTCGAGTACGGCTACCCTCGCGTCTCGGGACCTGCTCGATCTGCTGGCCTGAGGAATGAGGAGCAGATGACCCCCCTG
> M T P L

> R L R V E Y G Y P R V L R D L L D L L A .
8354 CGGATCGCGATGGTCAACATACCGTTCCGGTTGCCGAGCGACGAGCGGCAGTGGATCAGGTCCCGCCGAGGGGTACGGCGGGATCCAGTG
> R I A M V N I P F R L P S D E R Q W I T V P P Q G Y G I Q W
8446 GATCGTGGCCAACAAGATCAAGGGCCTGCTCGAACTCGGGCAGGAGGTTCCTGCTCGGTGCCCCGGGCAGTCCGCGTACGCATCCACGCC
> I V A N K I K G L L E L G H E V F L L G A P G S P R T H P R
8538 TGACCGTGGTGCCGGCGGCGAGCCGAGGACATCCGGGCATGGTTGAAGTCCGCTCCGGTGGACGTGCTCAACGACTACAGCTGCGGCAAG
> L T V V P A G E P E D I R A W L K S A P V D V V N D Y S C G K
8630 GTGGATCCGATCGAGTGCCTCCGGGGGTGCGCCTGGTGGCTCGCACCATGACACCCGCCCGTCTATCCGGCCGGGTGCGGTGACGC
> V D P I E L P P G V G L V A S H H M T T R P S Y P A G C V Y A
8722 CTCGAAGGCGCAGCGGGAGCAGTGCGGCGGGCGGACGCCCGGTATCCCGATCGGGGTGGATCCGTGCTCTACCGCCCGGGCGACC
> S K A Q R E Q C G G A D A P V I P I G V D P S L Y R P G D

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FIG.11A(8)

8814 GCAAGGACGACTTCTGCTCTTATGGGCGGATCTCCCGTTCAAGGGCGCGCTGGAGGCGGCGCGGTTGCCCCGGGCGCGCGCGG
>R K D D F L L F M G R I S P F K G A L E A A F A R A A G R R
8906 CTA CTGATGGCCGGTCCGGCCTGGGAGCCGGAGTACCTCGACCGGATCATGGGCCAGTACGGCGACACGTACCCCTCGTCGGCGAGGTGGG
>L L M A G P A W E P E Y L D R I M G E Y G D H V T L V G E V G
8998 GGGTCAGGAACGTATGACCTGCTCGCCACGGCGGTGCCATCCTGGTGCTCTCCAGCCGGTGCCCGGCCGTGGGGCGGCACGTGGTGCG
>G Q E R M D L L A T A A A I L V L S Q P V P G P W G G T W C
9090 AGCCGGGTGCGACCGTGGTGTCGAGGCGCGGCGGACGGCACCCCGGTGGTCGGCACGAGCAACGGTGCCTGGCGGAGATCGTGCCGGCC
>E P G A T V V S E A A A S G T P V V G T S N G C L A E I V P A
9182 GTCGGCGAGGTGGTGCTCGGCACCGCTTCGACGAGCGGGAGGCCGAGCGGTGCTGTCCGACTGCCGTGCCCCGCCAGCGCGGAA
>V G E V V G F G T G F D E R E A R A V L S R L P S P A Q A R K
9274 GGCCGCGATCCGGTGCTGGGGGCACGTGGAGATCGCCCGCGCTACGAGCGGTGTACCGCGACGTGCTGGCCGGCGCGCTGGTCCTGA
>A A I R C W G H V E I A R R Y E A V Y R D V L A G A R W S .
9365 GCCGGCCGGCGGGCTACGGTCGCGACCGTAGGGGTGCCCGCCGCGACGCGGAAGCGCGGTGTCGGCGGTCCGACACCGCGGCCCG
9457 GCCAGGTCAGTCCGGTCGTGCAGCCAGGTCGCGGTCGCGGTGCGTACCTCGACCGGTGCTCATGAACACCCAGGACGTACGCGCGG
< . S R D H L W P R P E P D T V E V P Q S M F V L V Y A R
9548 CGCGGCTGGTCCGTCTCGTTCGGGCGGCGTAGTGCGGCGCACGGAAGTCGTGCATGACCGCTCGCCCGGCCGACGGGCGAGCGACGCT
<R P Q D T E N P G A Y H P A R F D H M V A E G P R L P C A V S
9640 GTCCGTGTCGACCTCGTCCGTATCAGACCTTCGATGCGGTGCTGTTGATGTGATGGTGGGGAGCACCCCGCCCGGTGCAGGC
<D T D D V E D T M L G E I R D D H N I H H P L V G G R H L G
9732 CCGGCAGGTACTGGAGACAGCCGCTGGACACCGTCGCCTCGTCGAGCGGGTCCAGATGCTCAGGCCGCGACGGGACCGGGGTCCATG
<P L Y Q L C G S S V T A E D L P T W I S L G R R S W R P D M
9824 TACGCTCGTCTGGTCCACGGAGTGGTGCGCGGTAGCGGGCGGCTTGAGGATCGCGTGGCCGTAGAAGTCGAGTTCGTCTCGGGGAT
<Y A E D Q H W P T P A G Y R P P K L I A H G Y F D L E D E P I
9916 GTCGAGGAAGCGGAGCGATGGCCCGGATCGCGGAAGTGGCGGTCTCCACCAACTCCGGCAGGTATTTCTCGGCGCGACGATCTGCG
<D L F A S A I A R C R A F H A T E V L E P L Y K E P R V I Q P

FIG.11A(9)

10008 GGAGACGGGACGGCGGCGTCTGTCGCCACGGCCGGCGATGTCCCGGTAGTCGCCGGTGTCTGGGCGACGCGTGATCGGCGAAGAGCCGGTCTG
< L R A P A A D D G R G A I D R Y D G T D P S A H D A F L R D
10100 TAGGCGGCCGGAGCCAGGCGACCTCGGGCTGTCGGCGAGCTCGGGGAGAGTCACGAAGCCATCGCGCCGGTAAGCCTCCAGCCGACGGTC
<Y A A R L W A V E A D D A L Q P L T V F G D R R Y A E L R R D
10192 GACGACCTCGCACCAACAGTCCCGCATTTGACCACCTCTCGGAATAGCCTGTCCGCGAATAAACCATACGGTAGGAACAGCGCG
< V V E A G V T G V A M
10282 GCGATACCGTCCCGAGCGGGAATAGGGATTTCGACTAGTATTCGGTCCGCCCGCTGCCAGAACGGCACGCGCTCTCGATTGTCCATTTCAT
10374 CCCCCTGCGAGACTCGCCTCGATGTCTCGATGTGCGTGGGGGTTTGGGATGACCGGGCACAGCGCGTCTGCGCTGGACGTCTGGCGGGGT
> M T G H S A V A L D V G G V
10465 CGTCTACTACGACGAGCCGTTTCGAGCTGGCCTGCCAGGACACCTTCGACCGCCTCCAGGCCACCGACCCGACGCTCGACCTGCGTGCCT
> V Y Y D E P F E L A W L Q D T F D R L Q A T D P T L D L R A
10557 TTCTGGAGCACGTCGAGCGGTTCTACCACCTACGGCGAGGGCGACCCAAACCGCCGACCTGGCTCCACTCGGAGGCCGCCGCGCTGAGCTGG
>F L E H V E R F Y H Y G E G D P T G R T W L H S E A A L S W
10649 TCGCGGTCGCGCAGTCTGGGGCGAGTGGCCAGGAGATTCCCGGTGCCGTTTCGCGCGGTACACAGGCTGGCCAGGGAAC TACCCGTCGT
> S R V R Q S W G E L A Q E I P G A V R A V T R L A R E L P V V
10741 GATCGTGCCCAACGACCCCGAGTGCGCGGACGTACTGGCCCGGTGGCAGGTACGCCAGGTCTGCCGGGAGGTGCTCCTCGACTCCCTCG
> I V A N Q P P E C A D V L A R W Q V S Q V C R E V L L D S L
10833 TCGGGGTGGCCAAGCCCGACCCGCGCTGCTCGGGCTCGCCCTGCGGGCGGTGGCGATCCCGCCCGCGAGTTGCTGGTGGGCAACCGG
>V G V A K P D P A L L G L A L R R L A I P P A E L L V V G N R
10925 ACGGATCAGACGTCTGCCCCGCGCTCGGGCTCGGTTGCCCGTGGCGTTCTGTGCTGCCCGATCCGGCGTACCGCCGGCCGCCGGGCGGTCCA
>T D H D V L P A L G L G C P V A F V L P D P A Y R R P P G V H
11017 TCCGGACCTGGTCCGGGTCTACACGGAGCTGAGGGCGTTCCGCACCGGCTCCCCGCCCGGGACGCCCGGGTACCACCGTGGCGTCCCTGG
> P D L V R V Y T E L R A F R T G S P P A D A R V T T V A S L
11109 CGGCCCTGGCCGACTCTCCCTGACGAGTGCCACCCCGGTTTCGAACGCCGCGACCCGGCGGACTTTGACGAAGGAGTGCAGTTGCGACGCC
>A A L A D S P L T S A T P R S N A G T G G L .

FIG.11A(10)

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11200 CCGCAGCGGTGTCGGCGCCACGGCTTCATCGGCTCAGCCTCGTCTCCGCCCTGGCCGAGGCCGGGCATCCGGTGGCGCGCTTCAGCCG
11291 TGCCGCCCCACCCGTGTCGACGGCCGGCCCGCGGGCTCCGCGAGGCGCAGGTGCTACTTCCTCGCCGCCGGCTGAGCCCGGGCGC
11383 TGGCGGAGCAGCAACCGGAACGGGTGTCGGGAACGCGAGTTGTTGCTGGACGTGCTAAGTGCCTGGCGGGGTGGACACCGGCCGGTG
11475 TTGCTCTGGCCAGCTCGGGCGGGCGGTGTACACCGACGAGTGTGGCCGCCCTACCAAGAGCGGTGGCCACCGGGCCCGCTCGGCGTA
11567 CGGCCGGCGAAGCTCGGGCTGGAACAGGAGTGTGCGGCACACCGAGCGGTGCAGCCGGTGGTGACCCGGTGAACAACGTCTACGGTC
11659 CGGGGACGGCCGACCCCGGGTACGGTGTCTGTACACTGGCTGGAGGCCACCGTGC CGCGAGAGCCGATCCGGCTCTTCGGCGATCCG
11751 GCCGTGGTGGGACTACGTACAGTCGACGACGTACCGCGATCATGGAGGTTCATCGCGCAGCGGGCCGGTGACGGCAGCCGGACCGGT
11843 GCCCACGGTCGTGAACGTGGCTCGGGCTGCCACCTCCCTCGCCGAGTTGCTCCAGACGATGTCCACGGTGGCCGGTCTGAGCTGGAGG
11935 TCATCCGGGACGTCGCCCGGACGTCGACCATCGGGCACTGGCTCGACACCAACCTCGCCCGGAGACCTGGGCTGGCAGGCGCGGATC
12027 AGCCTCCCCGACGGCGTCGCCCAGTGTGGAGGCGCTCACCCGGGCGGGCGGGGGTTC CCGGGCCCGACCGTCAGCCCGGC
> S L P D G V R Q C W E A V L T R A G G P G S P A R P S A R
< . G P

12118 TCGGGAGAGCGTCTCGGGGGCGGAACCGCCGCAACCGGCCCTTCGCAGCAGTTCGTGGCTCAACCCGGCGGGGTGCGCCGGTGTAGCC
> L G R A S R G R E P P Q P R P S Q Q F V A Q P G G R R G V A
< E P S R R P P F R R L R A R R L L R H S L G A A T A A T Y G
junction marker

12210 GAGGGCCAGTGGCAGGGCAGCCGGGATTCGGGGCCGTACGGTGCCGTCCTCCATTCCTTGCGCAGGCCGGCCCGTGCCTGGTCCGTCCGG
> E G Q W Q G E P G F R G R T V P V P F L A Q A G P C L V P S G
< L A L P L A L R S E P A T R H R D W E K R L G A R A Q N R G A

12302 CCTGCACCGCCCTGCCAGTACGCCCCCGCAGCAGGTACCGGGGGGTACCGGGGGTTCAGCCGGCCCGGTGATGTCATGGGTGACC
> L A P P L P V R P P Q Q V P G G Q P A R V D V M G D
< E C R G Q W Y A R R L L Y R P T L R G P D I D H T V

12382 GCGTGGTCCGGGAGCAGTTGCTCGGGGGCGCGGGCGCTTCATGGCGCTGATGAAGGAGGTGTCCTCC
> R V V R E Q L L A G A G G L H G A D E G G V L
< A H D P L L Q E R A G A A K M A S I F S T D E

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FIG.11A(11)

12451 CCTGACTGGAGGTTGCCCCCGGTACGGCTGAGGGCCAGGTGCGAAATCCAACCCGTGGGCGTGCGCGAAC
>P .
<G S Q L N G G T R S L A L D F D L G H A H A F
12520 GCGGAGTCCACCCCATGCACGGCCCCAGATCTTGATGTTCCCTGGTCACGGTGCCAGCCGACAGGTGGAAC TGCCGGGA
<A S D V G M C A G W I K I N G Q D R H W G V L H F Q G S
junction marker
12603 GGTGACGTACCACGGCAGACGACGCGGGGGGGCCAGCCGGGTGCCGACCACTGCGCGCCGTGCGCAGGCTCTTGCGGACGGCGTCTGA
<T V Y W P L R L A P R A L R T G V V H A G D R L S K R V A D V
12695 CGGCAGCGCGTCGAGCCGACGTCGTCGACGAACATCAGATGGTGGTGGCGCCAGCGGGCGAGCATCGCGTTGCGGGAGGCCGACAGG
< A A A D L R V D D V F M L H H P W R A L M A N R S A S L
12787 CCATTGGTGGCACCGAGGATGCGCATGGTGCCGCGCGGCCGACCTCTCTGGCGACCTCTCCGCCTCGGCCGTGACGGGCCGCTCCAG
<G N T A G L I R M T G G A A R V E E A V E E A T V P R D L
12879 CAGGACGTAGTACTCGTCGCCGGAGAGCTGGGCCATGTTGTGCGCGAGGTGTTCTCTGACGTTCTCCACCCGGAACGCGCAGATCGCCACCA
<L V Y Y E D G S L Q A M N H A L H K R V N E V R F A C I A V V
12971 CCATCGGGTGGTCGACGGATCGCGGCTGACCACAGAGGGGTGTTTCGGCATCGTCCCTCGACATGAGCGTTGTGGGGCCGGCGGGGAGA
< M P H D S P D R S V V S A N N P M
13061 GCGGGCCACCGGATCGCGCTCCGCGGCAGCGTGCCGCGGCCCGGCCGCCACGGACAGGTGGCGCACCGCAGCGCGGGCGGGCGTCCGG
13153 TGAGCGGCCGGGGCGGAGCTCAGGCCGCTTCGTCCCTTGCTGACGGTCGGCGGCCAGGTGCCCGCCGCGAGGATGCCCCATCGCGTAGCCCTT
13245 CGCGATCAGGGCCGGCGTTGGGCACCTCGCAGGTTCTGCAACAGCTTGCTGACGTGGTACTCGACGCCCTGACGGCTGAGGTAGACCTTGT
13337 TGGCGATATGCACCGTCCGTTCCGCTGCGGCGATGCTTCGATGATGCGGCGTCCAGATCGGACAGTGAGAACTTGAGATTACAAACGCC
13429 CCTTGATTGTGGATCTGTGGCTGTACGCGGCCAGACGTATCGCCCGGACACCCCTTGAGTGCCGGTGGACGAGTGGTCGCTTCGGCT
13521 GGAAGACCGTCAGCGGGGGAAGCCGGGTGCCCCGCCACTCGTCGCTTCGCGCTTGCGGAGCTGTCTCAGTGTGCGGCGATGCCCCCGGCACG
13613 TAGCCCGCCTGACGGGCTGTGCGCTTGGGCTCCAACCTTCGGCAACCCATCGGTTGCGGCTGCACAGAACCAGCGGAGGAACATTGAGTTTC
13705 GAAGCCCTTCGCTACTGTGATCGACATCACTGGCGAAATGAAACCGACCGGATTTCGAGCCGATGTTACGGAAAGTGACAATCGGCTGGCC
13797 CTGTGCTCGCGTGAACTACCAATAGCCAAAAGCGTAGCGGGCCCACTGCGGAGCGTCCACCCCCGAGGATATGCCAGGCTTCCATG

FIG:11A(12)

13889 CAGAACTGGCAGGATCTTTTCATCTCAGCCGACCTGGCGACAAAACCCCTGCTCAAGACCATGAGTAAGCAGGCGGGAAATCCATGCAGT
13981 GACATGTGTCACTTTAGACAACCCAGCTCCAGCCAGGCCACCAACCTGACAAAAGGGCGGAATCGCGACCAGAGCGACACAGCACATTC
14073 CTAGGGGATTCTTAGTCTGGCGAGGTGATCCCCACCCGTCATCAATTGCCCGAACAATTTGCCACCCGTCAAGATCAACCACTCCG
14165 CACCGTGAGCAGGCCGACCGTCCGGCAATGCGAACGACGACGTCCACCCGTCCTCCGGTAGCCTACCGCCGTGGGGGGGCACGGGCCGGA
14257 CACCGTCGGCGTGTGATCAGCGGTGCTGCGCGGTGTGCGCCCGCGGGGACCGGCATCGCGCGGGGCCGACACGAAGATCTCCG
14349 GCGACCTGTCAGCCCTGCAAGCGGACCGGATCGCGCGGGGCGGGAACCAACCCGACGGTTCAGCGCCGGGACCGATCGGGAAGCCGACT
< . R R S R D P L R S
14440 CGCGGCCTCGTCCAGAGCCCGCCACCGCATCCCGCAGCGATCGTGGGGCGCCACCCGAGCAGGTCACGCGGGGCCCGGTCGACGC
< A A E D W L G G V A D R L S R R P R W G L L D R A P G P D V R
14532 GGGCCAGTCGACGACCTCCACGAGCGGGCGGATCCGGCAACTCCACCACCTCGGTGGCACCCCGCTCACCTCGATCAACATCTCCACG
< A W D V V E V S G P R D P L E V V E T P V G S V E I L M E V
14624 AGGAGCGGACCGGAACGGCCTCCCCCGCCACGCCGATCACCCGCCCGGTGACGGACTCCCGCTGGCGCGACACCCGCTCGGGCGAC
< L S R V P V A E G R G V G I V R G T V S E R T A S V V A E A V
14716 GTCCCGCACGTCGACGTAGTCCCGGTGGCGCGCAACGGAGACAATCCACCCTGGCCGACCGGTGCGGGCCCGCGCTCGACCAAGGCGAA
< D R V D V Y D R H A R L P S L E V R A S R D R G A A D V L R V
14808 CGACGACCCGCCCAACAGGCTGTCGGGTGGCACGCCCGGACCCACACGTTTCGGAGCCGACACCGTCGCGTCCACCGAGCCGGCCCGC
< V V R G L L S D P P V G P G V V N A L R L V T A D V S G A R
14900 GTCGCCGCGAGCACGGCCTGGGTGGCGGCCAGCTTCGCCCTGCCGTACATGCTCTCCGGCTGGGTGGGCACCGTGGCACCCGGGGAGCCCC
< T A A L V A Q T A A L K A R G Y M S E P Q T P V T A G A P A G
14992 GGGTGGCTCTGGACGCGTTCCAGGACCGAGCGAGGTGCACAGCCTGGGCCGGCAACGGGTGCGCTCCAGCGCCGCGGTGACACTCCACG
< P P E Q V R E L V S G L H V L R P R C R T R E L A A T V S W T
15084 TCGGGATCGTCAGCTCGACGGCAGCTCGGCGTCCGTACAGTTCCACTTGCCGCCGGTGGCGTTGACCACCGCTCGGGCTGCTCGGGCGTCG
< P I T C S S P L E A D T L N W K G G T A N V V A D P Q E A D

FIG.11A(13)

15176 AACACGGGGCCAGCGGGGGCTCCAGGGTGGCGACGTCCAGGCCCCGGGCCCGGTACGGCAGCCCCGCCGACGGGACGGCGGGGCCAA
<F V A A L A A P E L T A V D L A R A R Y P L G A S P V R A L
15268 CACGAGGACGTGTCGCCCCGGGGCAAGCGGGCTCACGTACGCCCGACGAAGCCGTACCAACGACGACCAACGACAGCGCGCGC
<V L V D D G R A A L A A S V H R G V F G T G G V V V R A G
15360 CCATCGTACCTCCTGGGGATCAGTCTGTGGCGGGGGCTCCAGGCGACCGCCGGCCCCCTGACAGGTACGGGGGCGCGCAACAC
<M < . D R A G A A D L R G G P G Q C T V P A R L V
15449 CCTGGCCCCGTGCGAACCTCGTCCAGAGCGGGGGCGGGATCGCCGTACCTCCTCGCCGGCTGACCGGCGGTGACGGCGGGA
<R A R D R V E D L L R A R A R I A T V E E A P Q G A T V A R V
15541 CGAACTCTGCATCGTGTGACGAACTGTCCTCGGCGGGAAGGTCAAGTCCCGCGTCTCGTCTGCCGCTCCACCCGACCCACCGGGTGC
<F E R M T N V F Q D E A P F T L E R T E D Q R E V R V P H
15633 CAGGCGGGGTGTACGCCGGTTCGACGACGATCCGGCGGGCGCTTCCCCAGAGCTGGTACTCGACCCGGTAGGAGTGTCTCGAAACC
<W A P P T Y A R D V V I R G A S G W L Q Y E C R Y S H E F G
15725 GAAGCGATCTGTGCGTCCGCCCGTCCGGGTACACAACAGCGGGCACCCGAAACGTCCACGCCGATCGGGGTCTCCCGGAGGGTGG
<F A I Q A T R G D P T C L L A A G S V D V G R D P D E R L T A
15817 CCGCCACCACCTCCGGCTCCTCCGGCAGGAAGAACCGGGCGGCCCAACGGGTAGACGCCCAGATCCAGCAGCGCTCCGCCACCCGCCTCG
<A V V E P E P L F F R A A G L P Y V G L D L L A G G L E
15909 GGTGGTAACGGATGTCGCCCGCAGGCAGCGGGGAAACCCGAAGACGCCGGAGACCATCCGCAGCTCGCCGATCTCGCCGGCGCGACCAT
<P R Y R I D G A P L P P F G F V G S V M R L E G I E G A A V M
16001 CCGGCGCACGAAGTGTGCACCCCATGTCCGAGGAAGGTGAGGTGTCCATCAACACGAGCCACGCGACCGGGCCTGGGTGAGCACCGCG
<R R V F H H V G H R L F T L N D M L V L G R S R A Q T L V A A
16093 CGGTGTCAGCAGCGGGTGTGAGCGCTTCTCCACGACGTGTTTGCCCGCGGCCAGGGCGGTTCGATCCAGGTGTGGTGCAGCCCG
<T D V L R T T L P K E V L V H K G A A L A R E I W T H H L G
16185 GTCGGCAGCGGAATGTAGACGGCATCGATGTCGGGGGTGAGAACGGACTGGTAGCCCTCGGCGGGCGGCACCCGAACCTCCGCGGGCAA
<T P L P I Y V A D I D P R D L V S Q Y G E A A C G F E A A F

FIG.11A(14)

16277 GGCGCGCGCTTGGCCAGTTCGCGCGCGCGACACACGAGCTCCGCCTCCGGGACCCGCCTGATCGCCGGCAGGGCACGGCGGCGCGGA
< A R A K A L E R A A V V L E A E P V R R I A P L A R R A I
16369 TGTGGCGCAGCCGAGAACCCGATGCGGACCGTCACTCCGCCATCGGGTCAACACAGGCTGCGCAGGCAGGCCAGCAAGCTGCGGGCC
< D A C G K V G I R V T M E A M < · W L S R L C A L L S R A
16459 TCGATGTTGAGGTAGCCGTGCCGAGCAGGGCCTCCAGCTGGCGCACCGTCAACCCAGCAGAACTCGTCCGGCACCTCGGTGCGGAAGTC
< E I N L Y Y G H R L L A E L Q R V T V W C F E D P V E T P F D
16551 GTCGCGCGCTGACACGAGGTAACGGTTCTCCGACCGGTAGAATCGCCCGCCCTCCTCGGTGAGCACGGTGTCTAGAGACACGCTCGG
< D G A D V L L Y R N E S R Y F R G G E T L V T D Y L V R E P
16643 GGGCGGCTTCAGCACCTCGGCCAGGAACAGTGGTGGGGGCGGGCTGGTTGTCCGGGATGCACTGCACCGTTGGGCCCATCTCCATCGCG
< A A E L V E A L F L P R P G P Q N D P I C Q V T P G M E M A
16735 TCGAGCAGCCCGCTGGTAGCGCGGTGCACACGAGGTGCGCCACTCCGTGATTTCTTGACCAGGAAGCGACACGCCCGGTGCGG
< D L L G A Q Y R A H V L L H A V G D I E K V L G A V V G R H R
16827 CGGATACAACAGCGGTGACTCCACCCGGTCACCTCGCGTTGTGATGCGCACCGTGACGCCGACACGGAGGAGTGCCGGCCGTCGTCCC
< P Y L L P Q S W G T V E R N D I R V T V G V V S F H R G D D R
16919 GCGGATCCGTCGCGGTGTGCCGCCAGTCCGGCAGCCCTCGTAGCGGCACCCGCCGACCGGTCACTCGTGCCGGCCCTTGGCCCCGGTG
< A I G D A T H R W D P L G R L P V R R V T M E H R G K A G T
17011 AACCAGCTCAACACCGACACAGGTGTTGGCGGCGGGGGCGCCGCCGAGCGCACGATCGCCGCCACCGCGCGGACGACGCGGCGCTC
< F W S L V S V L D H R G P A G A A S R V I A A V A P S S P A E
17103 GGTCCTCTGGCGCGCGGTAGAAGGCCGAGGGCAGACATGACAGCACCGTACGCGTGTCCATGTTGACCAGGCCGTCCACCCGACGACGG
< T E Q A A A Y F A S P L C S L V T R T D M N V L G D V R L L A
17195 CGAGCAGTTCGCGCAGCGGGAGCCACCGGTGGTAGTCGCGCGCGGCACGTCTCTGTCGACCTGGACCACCATGTTCCGGTTGCGCTTGCGC
< L L E R L P L W R H Y D G A P V D E D V Q V V M N R N R K R
17287 AGGAACAGGAGCCCTGCTCCGACTGCAGGACGTCAACACGACCCCGCCGCGGGGTGAAGTAGTCGAGGTACTTCGTGCGCGC
< L F W S G Q E S Q L V D V L V R G A G P R T F Y D L Y K T G G

FIG.11A(15)

17379 GCCACGGTGCACCGGGTGTAGTTGCTCCGGGTGGCTGCACCGTCCGGCAGAGCTGCATGACGTTGATGTTGCCGGGCTCCACCTTGGCCT
< G R H V R T Y N S R T A Q V T P S L Q M V N I N G P E V K A Q
17471 GGAGCAGGCAGTACGGTGTCCCGTCGACGACCTTGACGAGCATGCCGAGGATGCCGATCTCCGGCTGGTTGATGATCGGGCTGGTGCCATTCCG
< L L C Y P T G D V V K V L M G L I G I E P Q N I I P Q H W E
17563 CGCACCGCGCGTAGGTGGTCTGGACGTGACGCCCTCGATCACGAAGAACCGGCCGCTCTCGTCCCGAGGTTGCCGGTCACCGGGTCGAA
< R V A G Y T T Q V H L G E I V F F R G S E H G L N G T V P D F
17655 CGCCACCCGGGCAGCCGGTCCAGCGGCACGGGTCCACCCGGCAGTAGTGCACCGGGTCCGCTCGCGGAACCAAGGAGGAAGTCCGGCC
< A W G P L R D L P V R D V E C Y T S R T R E A F W S L F D P R
17747 GGACCCCTCGGCGTGCAACGCCGACCAAGCGCGCTCGACCGGGCCGGGTGCGGGCCCGCTCCGGGTCAGCAACGGCCCGTCG
< V G E A H L A S W S G G D V P G P R H P G A D R T L L P G D
17839 GCGCGGACCTTCGGGTCCGGCGACGAATGCTCACCAAGCTCGGCCAGTTCGGCGGAAGGCGTGGGAAGACCCGTCGTCGCGCCAA
< A R V K P D P S S D S V
< · W L E A L E A S F A H S S G D T D A L
17930 CAGGCGCAGATCGCTGTCGACCATCATGGCGACCATCTCCTCGAAGGAGACGGAGGTTTCCAGCCGAGCCGCTGGCGGGCCTTCGTCCGAT
< L R L D S D V M M A V M E E F S V S P K W G L R Q R A K T P D
18022 CCGCGCAGACGCTCGACCTCGGCGGGCCGGATGAGCGACTCGTCCACCACCGTGGTCCCGCCAGTTGAGGCCCCACGTGGCGGAAGGCC
< A C L L E V E A P R I L S E D V V V H D R W N L G V H A F A
18114 GCCTCGACGACTCGCGGACGCTGTGCGTGACCCCGTGGCGAGGACGTAGTCTCCGGCTCGTCTGGGCCAGCATCAGGACCATGCCCCG
< A E V L E R V S H T V G T G L V Y D E P E D Q A L M L V M G R
18206 CACGTAGTCCCCGGAAGCCCCAGTCCCGCTCGGCGGAGAGGTTGCCAGGCGAAGCGAGCTGCGAATGCCAGCTTCACCGCCGCCACGC
< V Y D G A F G W D R E A S L N G L R L S S R I G L K V A A V G
18298 CCAGCGACACCTTCGGGTGACGAACTCGGGACCACGACCGGTGATTCTGTGTTGAACAGAATGCCGGAGACGGCATACATGCCGTACGAC
< L S V K R T V F E P G R V P S E H N F L I G S V A Y M G Y S
18390 TCACGGTAGTTCTGCACCATGTAATGCCCGAACGCCCTTGGCCGCGCGCTACGCGGATGGAACGGGGTCAGCTCATTTGGACGGG
< E R Y N Q V M Y H G F A K A A G Y P S R P H F P T L E N Q V P

FIG.11A(16)

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18482 CTCCCGCACCTTGCCGAACATCTCCGACGAAGACGCCTGATAAAAGCGCGGTGACCGGGTGCGGGACTCGGGAATCCGACAGGCCCCCA
    < E R V K G F M E S S A Q Y F R P Q G A A P S R S D S L G G V
18574 CGATCCGAAGGCTTCGAGCATCGGAGCACACCATGCCGGTGACCTCCGCCGTGTTGGTGGACTGCCGCCACGACACCGGCACGTACGAC
    < I R L A E L M R L V G M G T V E A T T T S Q R W S V P V Y S
18666 AGCGCGCGAGGTTGTAGACCTCGTCGGCGCGGCTTCGATCGCGGCCACCAAGGCTCGTCTGATCCAGAAGGTGCGCGTGATCAGCTT
    < L A G L N Y V E D P A A R E I A A V L S T Q D L L D G S I L K
18758 GACCGCTGGATCAGGTTGCCGAAGGTCGGACCGAGGGCGGGTCTGCCCGCGCACCAATCCAAATACCTCGTATCCGGACTGAAGCAGGT
    < V A P D P Q R L S R V S P A T Q G R V L G F V E Y G S Q L L H
18850 GCTCCGCGAGATACGTGCCGTCTGGCCGGTAATTCAGTGATCAGCGCCCGCGTGTCAAGGTAGTCTCCAGCCGTGAAGCCACCTGGCC
    < E A L Y T G D Q G T I G T I L A R R T L T T E L R S A V
18941 GAGGCGTGACCTCGCGCCGATGGCGGACCAAGATCCGCCCTTCGAAATGGGGTCGGATCTCCCGTACCGCGCTCACGGTACGCGAATCT
19033 CCAAGCGGATTACGCGACCCGGAAGCAATATAGGGAGGTTACTAGTAGTACTTCCGGCGGCCGCGAGCAGCCCGCCGACCGGCA
19125 GGATCGCCCCGTTGGCCGGGACCCATCCCGGACACCTTCCACCGAAGCTCTTCGGGATCGTCGCCCGCCGATCGGAATGCTTGACTCC
19217 ACCGTTTTGTCCCCCTAACGTGCGGAGGCTGCCAGCCGCCCGGAGCCGGGCCGGTTACGAAGGCGCCAACTTCCGGTGAGAGAGCAG
19309 GGCTCATGTGCGAGAGCCGGCCCGCGCGCAGCACCCCCAGCCCGCTGCCACGTGCGCGGCCCATGGTCGCGTTGGTCGCGGTGATGAT
    > M V A L V A V M I
19400 CCCGATGGTGTGGCCACCCCTCGACAACACCATCATCGGCACCGCACTGCCACCGTGGTCGGCGAGTTGGCGGCCCTCAGCACGCTCTCCT
    > P M V L A T L D N T I I G T A L P T V V G E L G G L S T L S
19492 GGGTGATCACCTCGTACACGCTGGCCACGGCCGCTCCACGCCGCTCGGGCAAGCTCGCCGACATGTACGGCGGCAAGGTGGTCTTCGTG
    > W V I T S Y T L A T A S T P V W G K L A D M Y G G K V V F V
19584 GCCACGCTGGTCGTGTTCTGGCCGGGTCGCTGCTCGGGCATGGCGCAGAGCATCACCCAGTGACCGTCTTCGGGGCCGTGCACGGGCT
    > A T L V V F L A G S L L S G M A Q S I T Q L T V F R A V H G L
19676 CGGCGGGGCGGCTGATGGTCTGCGCGTTCCGCCATCATGGTGGAGGTTCTCGCCGGCCCTGACCTGCCCAAGTACCAGGGCATCATGTGCG
    > G A G G L M V C A F A I M V E V L A G P D L P K Y Q G I M S

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FIG.11A(17)

19768 CGACCATGGGCTGACCATGGTGGCGGGCCCGCTCGTCGGGGCCCTGATCACCGATGAGTCGGCTGGCGCTGGTGTCTTACATCAACCTG
 >A T M G L T M V A G P L V G G L I T D E L G W R W C F Y I N L
 19860 CCGATCGGGGGCGGTGCGCTGCTCATCGTGGTGTGATGACACCTGCCGCGCGACACACCAAGGCCCGGATCGATTACGCGGGTGTCTG
 >P I G A V A L L I V V L M M H L P R R H T K A R I D Y A G A A
 19952 CCTGCTACCGTGGTCAGTTCGTGCGTGTGACACACCTGGGGCGGCATCACCTACCCCTGGCGGTCTCCGATGATCCTGGGGCTGG
 >L L T V V S S C V V L V T T W G G I T Y P W A S P M I L G L
 20044 TCGCGCTCGGGGTGCTGACCTGCGCGCTCTTGTGGTGTGAGCGAGCGGTGGCCGAGCGGTGGTGCCCTGGCCATGTTCCGCAGCCTG
 >V A L G V L T C A L F V V V E R R V A E P L V P L A M F R S L
 20136 AACTTCACCTGAGCACCTCATCGCCTTCTGGTCGGCTTCGCCCTCATCGCGGGGTGACCTTCCTGGCCCTGTTCCAGCAGGCGGTGCA
 >N F T L S T L I A F L V G F A L I A G L T F L A L F Q Q A V Q
 20228 GGGTGCCTCCGCTCCGACTCCGGCTGTGCTGCCCTGCTGTCTCATGGCGGGGTCAACGTGGTCGGGGTGCCTGATGAGCG
 >G A S A S D S G L L L P L L S M A A V N V V G G R L M S
 20320 GCGGGCTTCTACCGGTGCTGATGCTCGCGGTGCGGGCTGATGACCTGAGCTGTCTTCGCCCTGATGGACGTGGGCACCCAGC
 >G G R S Y R L L M L A G A A L M T L S L L L F A L M D V G T S
 20412 CCGACGGTCACCGGATCCCCATGGTCGGCTTCGGCGCAGGGCTGGGGTGTCTATGCAGACCAGCCTGATGGTGGCGCTGAGCAGCGTGGA
 >R T V T A I P M V G F G A G L G L L M Q T S L M V A L S S V E
 20504 GATAGGAACCTCGGGTGGCCGCTCCACGTCCACGCTCTCCGCACCATCGGTGGGGCGGTGGGGCGTCCGCGACGGTCTCGCTGTTCT
 >M R N L G V A A S T S T L F R T I G G A V G A S A T V S L F
 20596 CCGTGGGGTGCAGTCGGCGCTGGCCGATCGGGGGGTGCGCGACGTGGCTGACCTCCTCGGCCACTCCGCGGGCTGGACGCCCGGGGCTG
 >S V R V Q S A L A D R G V A D V A D L L G H S A R L D A A G L
 20688 GCCCAACTCCCCGGCGCTCCGTGTCCACTTCATGCACGGGTGGCTCCGGCACCCGGTGGGCTTCTGATGACCGTGTGGCGGGGCT
 >A Q L P R A V R V H F M H A V A S G T R W A F L M T V L A G L
 20780 GATCTGCTCGGGCGGTGGTTCTGCGCGGGGTACCCCGTTGACGTGGCACCGGTGGCACCCGACCGGCGCGGACGTGCGCGCGC
 >I C V A A A W F L R R V T P L T S A P V A P E P A R D V A A

FIG.11A(18)

20872 CCGCCGCCAGCGGGCGCGCGGAAC TACTAGCGGATTCCTAGGGTTCTCGTCGACGGTAGAGCTGAATTCACCGGGCGACCTAACCA
 >P A A S S G R A P N Y .
 20963 TTCTTTTCGGCATCCGGAATCCGTCCATTCCCTGTCTGGCGATGGTCGACGGCGGCCCGTCCGAGCGGACAGACAGATTCTCGGAT
 21055 TGGAGCTCGATGTCCAGCAAGATCCTAGTCATCGGTGGAGGTCCGGCCGGATCCACGGCCGCCGCGTGTCTGCCCGATCGGGGCTGTCTG
 >M S S K I L V I G G P A G S T A A A L L A R S G L S
 21145 GTGACGCTCCTGGAAAAGGAGACGTTCCCGCGATACCACATCGGCGAGTCGATCGCTCCTCGTGCCGCACCATCGTCGATTTCTGGGGCGC
 >V T L L E K E T F P R Y H I G E S I A S S C R T I V D F V G A
 21237 TCTCGACGAGGTCGACTCGCGGGGCTACCCGCAAGAACGCGGTCTGCTGCGCTGGGGCAACGAGGACTGGGCCATCGACTGGGCCAAGA
 >L D E V D S R G Y P Q K N G V L L R W G N E D W A I D W A K
 21329 TCTTCGGTCCGGGCGTGGGTCTGGCAGGTCGACCGGGACGACTTCGACCACGTCCTGCTCAACAACGCCGGCAAGCAGGGCGCAAGATC
 >I F G P G V R S W Q V D R D D F D H V L L N N A G K Q G A K I
 21421 ATCCAGGGCGGGCTGTCAAGCGGGTGTTCGACGGTGAGCGGGCCACCGCCGCCGAGTGGTTCGACCCCGAGTCGGGTGAGGTCCGCAC
 >I Q G A A V K R V L F D G E R A T A A E W F D P E S G E V R T
 21513 CATCGATTCGACTACGTGGTCGACGCGTCCGGCGGGCGGGGTGATCCCGTCCAGCACTTCAAGCACCGGGCGCCCAACCGAGACGTTCA
 >I D F D Y V V D A S G R A G L I P S Q H F K H R R P T E T F
 21605 AGAACGTGGCCATCTGGGGCTACTGGCAGGGTGGCTCGCTGCTGCCGAAC TCTCCCTCCGGCGGGATCAACGTCA TCTCCGCGCCCGACGGC
 >K N V A I W G Y W Q G G S L L P N S P S G G I N V I S A P D G
 21697 TGGTACTGGGTCA TCCGCTGCGCGGGCGACCGGTACAGCATCGGCTTCGCTGCCCACCAAGAGCCGCTTCTGGAGCGGCGCAAGGAGCACGC
 >W Y W V I P L R G D R Y S I G F V C H Q S R F L E R R K E H A
 21789 CTCGCTGGAGGACATGCTCGCCGCACTGGTACAGGAGTCCCCGACCGTGC GCGGGCTGACGGCGAACGGGACGTACCA GCGGGCGTGC GGG
 >S L E D M L A A L V Q E S P T V R G L T A N G T Y Q P G V R
 21881 TGGAGCAGGACTTCTCGTACATCTCCGACAGCTTCTGCGGGCCCCGGCTACTTCGCGGGCGGGGACTCCGCTGCTTCTTGACCCACTGCTG
 >V E Q D F S Y I S D S F C G P G Y F A A G D S A C F L D P L L

FIG.11A(19)

21973 TCCACCGGGGTGCACCTCGCCCTCTACAGCGGCATGCTCGCCTCGGGGTCCATCTTGGCCACCATCCACGGTGACGTACCCGAGGAGGAGGC
 > S T G V H L A L Y S G M L A S A S I L A T I H G D V T E E A
 22065 GCGGGGTTCTACGAGTCCCTTACCGCAACGCTTACCAGCGCTGTTCACCCTCGTCGCCGGCGTCTACCAGCAGCAGGCGCGCAAGAGGG
 > R A F Y E S L Y R N A Y Q R L F T L V A G V Y Q Q A G K R
 22157 CATACTTCGGCTGGCCGACGCGTGGTGACGACAGCGGGAACCCGAGTACGAGAAGGTAGACGGGGCCCGCGCTTCGCCCAGCTCGTC
 > A Y F G L A D A L V H D S G E P E Y E K V D G A R A F A Q L V
 22249 GCCGGCCTCGCCGACCTGGACGACGCGGGGAGGACGGCAGCAGCACCGCGGGCGGCACCGGGGAGCAGGACAACCTCCGTCCGGCA
 > A G L A D L D A A E G R H D S T A A A A P A E Q D N S V R Q
 22341 GCTCTTCTGGCCGCGAGGAGGCCCGCGGATGGCCGACGGCGCACGCGAGCGCCCGGTACGCGAGGCGCGGGCAAGCTCGACAGCC
 > L F L A A E A R R M A D A R T P S A P V S E A P G K L D S
 22433 ACGACCTCTTCGACTCGGCAACCGGCCTTACCTGGTCAACACCCCGCACTGGGGATCCGCCGGGCCAAGCCGGCCGACACGACGGCGGG
 > H D L F D S A T G L Y L V T T P R L G I R R A K P A D T Q A A
 22525 GCAGAGCAGTCTGCCTGAGGTTCCACCCCTGGTGGCCCCCGGCCGACCGCGCGGTCCGGGGGTGCTCAACCCCTCCCACCAACATCCG
 > A E Q S A .
 22616 GCATCCGGTCCGGCGGCTGAGCAGGGGACGCGCACCGACTCCGGCCCGTCACATGGACAAGGTACCTCTCCCGTGTGAACAGACGACA
 22708 GTTGCTCGCCCTCGGCAGCTGGCCGCGGAGGACCGTCACTGTCACGCTCCCTCAGACGGGACGCGCAGGCCGCCAGCGGCACCGGC
 > M S R S L R R D A Q A Q A A P A
 22798 GTCGCCCCCAACCCGCACGCCGGGCACGCCGCCCGGTGCCAGCCGGGTACGACGACCACCGTCCGGTACCCCGTTACCCGAGCCGA
 > S P A N P H A G H A A P V P S R V S T T T V A V T P F T E P
 22890 TGCCCGTCCCGCGGCTGACCCCGGTCTCCCGCGCGGACGGCATCGACGTCTACGAGATCCCCATCCGGCCGGCAGGTGCAGATCCTG
 > M P V P P R L T P V S R R D G I D V Y E I P I R P A Q V Q I L
 22982 CCCGGCTGCTACGCCCGCCTACACCTACGCCGGTTCCTTCGTGGCCCCACCATCCGGGGCCGACGGGGCCCGCGGTGCGGATCACCTA
 < P G L L T P A Y T Y A G S F V G P T I R A R T G R P V R I T Y
 23074 CACCAACGGGCTCGACACCCACGCCAACGTGCACCTGCACGGGGGACGTGCCGGGCCACCGGACGGTCAACCCGATGGACCTGATCCCGC
 > T N G L D T H A N V H L H G G H V P A T S D G H P M D L I P

FIG.11A(20)

23166 CGGGGGCTGAAGGTCTACGACTACCCGAACCTTCAGCGGGGGCGACGCTCTGGTACCAGCACACCCACGCCTACGAGGGCCGACCAC
 >P G G S K V Y D Y P N L Q R G A T L W Y H D H T H A Y E A D H
 23258 GTCTACCGGGACTGCACGGCTTCTATCTGATCGACGACCGGGCCGAGCATCACCTGGCGCTGCCCGCCGGCAAGTACGACGTGCCGATCAT
 >V Y R G L H G F Y L I D D P A E H H L R L P A G K Y D V P I M
 23350 GCTGCGCAACGCCAGTTCGACGACTCCGGCGCCCTCGTCTTCGGCCACCGGACGACCGGGTCACCATCTTGGCGAACGGCAAGGCCACG
 >L R N A Q F D D S G A L V F G H P D D R V T I L A N G K A Q
 23442 CCTACTTCGAGGTGGCCCCGCGCAGGTACCGGTTCCGCCTGCTCAACGGGGCGCTGAAGCACGTCTCCGGCTCAACCTGGGCGGCGAACCG
 >P Y F E V A P R R Y R F R L L N A A L K H V F R L N L G G E P
 23534 CTCACCCGCATGCCACGGACGGCGGGCTGCTGCCCGCCCCACCAGTCACACCGAGCTGGCGCTCTCTCCGGGGAGCGGGTCGAGATTGT
 >L T R I A T D G G L L P A P T S H T E L A L S S G E R V E I V
 23626 GATCGACTTCGCCGAGCAGCAGGGCGGGCGGTCTACCTCTACGACGGGGACAACCCGATCTCGCTTCGACGTGTCGTCCCGGGCGG
 >I D F A E H A G G G P V Y L Y D G D N P I L R F D V S S R A
 23718 TCACCGACCCAGCGGGTGCCGGTCAACCCTGCGGGCACTGCCCCGATGGGCACGCCGACCGTGGAGCGCACCGTGTCTGATGAGCTTCGAC
 >V T D P S R V P V T L R A L P P M G T P T V E R T V S M S F D
 23810 ATGTGGCCCGCCCCGATCGCGTCA TGACGGCAACCGTTTCGACCCCTCTCCGGTGGACGTACAGGTCAAGCGGGGACGACCGAGAT
 >M S A R P P I A L M D G K P F D P L R V D V Q V K R G S T E I
 23902 CTGGAACGTGGTCAACGCGGATACCGATCCGTTCCCTTCGACCATCCGTTCCACCTGCACCTGGTGACGTTCCGGGTGCTCGGCCGCGACG
 >W N V V N A D T D P F P F D H P F H L H L V T F R V L G R D
 23994 GCGGGCCCGCCGCGGAGGACGCCGGGCTCAAGGACACCGTCTACGTCTGCCCAAGGGGTCTGTCAAGATCCAGGTACCTTCGCCACG
 >G G P P A P E D A G L K D T V Y V S P K G S V K I Q V T F A T
 24086 CCGTACCTCGGGCAGTACGTCTACCACTGCCACTACCTGGAGCACCTCGTCGCTGGGGATGATGGCCCCAGCTGGAGGTTGTGCCCTGAGGGC
 >P Y L G Q Y V Y H C H Y L E H S S L G M M A Q L E V V P
 24177 TCAGCCGTGCAGGTGACGATCGAGGGGTGGGGCGCCGAACAGGCTGACCGGGCCGACGTGCCCCACCCCGGCGGGCGGGCCAGG
 <· G H L D V I S P H A G F L S V P R V D G V G F G A A R A L

FIG.11A(21)

24268 TCGGCCTGGTCGGCGAACTCGTGCAGCAGCAGTACCGCCCGCCGCGCTGACCGTCAACCCGGCGCAGCTCCGCGAAGAGCGCGCGGAATC
<D A Q D A F E H L L L V A R G G D V T V R R L E A F L R G S D
24360 ACCGGCGAGCACGCCCGCGCTGCACCTGCCGTCCAGGGCGGATTGCTGACCACCCGGTCCACCCGACCGGTCCGACGGCAATCGTC
<G A L V G R A Q V Q R D W P P N S V V R D V R G T R L P L R G
24452 CGGCGTCGGCGACGCCAGGTGACGGGGCCCCGACGCCGCCGAGTTGGCGACGGCGCGCCGACCGTCTCCGGTCTGTTGTCGAGCGG
< A D A V A W T V R A G S A A S N A V A A G V T E P D H D S G
24544 AACAGCACGCCCGCGTGCCAGCCCGGCTGCCTCCACGGGGATCGTGCCGGTGCCGACGACGATCGCCACCGCATCCCGGGGGCGGAT
<F L V A G P A L G A A E V P I T G T G C C P D A V L M G P R I
24636 GCCGGCCAGCCAGCCAGCGCGCGGAGCGCGGATGCAGGGTCCCGGGCTGGACGACCGCTTGTAGGCCCGCCGGTGACGGCGCGT
<G A L W A L A A A L P P H L T G P T S S R K Y A R R H L P R D
24728 CGGCCACCGTACCGCCAGCGTGCCTGGGTGCCCTGCACGGTGACCCGACGACAGCCGCCCTCCGGCGGGGCTCGCCGCCGCGGGCGG
< A V R V A L T A Q T G E V T V R L S L G G E P P A E G G R R
24820 GAGTGTAGCGCAACCGAGCGGGCCACCGGTGCCGCCCCACGGCGTCTCGATGTCGTACCGTTGTAGTTGCGGCGGCGAGGAAGGA
<S H Y R L G L A A V A H R G V A D E I D Y R N Y N R R G L F S
24912 GCGCGCAGCTCCACGGTCGCCGGCCCGCCGCGACGCCGAGCGGGCGCGGCGGCGCAGCACCGCGGCGCGCCGCCCGCGCGCCAGCC
<A A V D V T A P R G P V G C A A R A P L V A P L A A R A L R
25004 GGGTAAGGCGCCAGGTCCGCCTTGGTGTGCCGACGCCGTGGCGACGGCGACGAGCAAGTCTGACGGTACGACGATCCAGC
< T F A A L D A K T H G V G D A V A V L L F L D D V T R L D L
25096 AGGCGCGCTCCGCGTGGCGGGAGAACACACCTCGCGGTGCCGGGTGCTCGACCCGGCGAGGCCCGCTCTCGATCTCTTGGGC
<L R P E A S A A S F W V E R H R R H E V R G L G R E I E Q A
25188 GGCCACCTCCTCCAGCCCTCGCAGGGTCGTGCCATGAAGCGCACCGTCAACGTCGCGCGATCCTCTCCCGCGGGTCTCCCGCGCCG
< A V E E L G R L T R A M
25278 GTCCGGCGCGTCCGCGAGCCTACCCACCGCACCCCGCGCGGACGACCGCGACCGCGACCGCGCGGGGAGCGGACGCGCGA
25370 CCGGACCCGCCAAGACTAGTGAACCTCTATAGGAATTCGCGTGCCCGCTTCATAGGGTCCGAAGGGGTAAATGGAACCGTCCGGCACCGGA

25462 CGGCTCGTTTTCTTCCCCCAATTCCGTCGTCGACCTGAGCCGTGCGCAGGGAAGGCCGAGGCCGAGCAGTTCGAGCAGTTGATCGGTCGATG
 > M
 25553 CCGCACGGGCCCCGTGCGCCGAAATCGTGGAGATTGCGCAGTGGTACACCGGATCTGTTTCATCGGGCCGCTCGGGCCCTTCGTCCCCGCCGAC
 > P H G P V R R N R G D C A V R T P D L F I G A V G A F V P P T
 25645 GGTGAGCGTCGAGTGGCGGATCGACCGCGGTCTTTACTCCCGCAGCAGGTGGAGCTGCACGAGCTGGCGGGCACGGCCATCGCCGGCGACC
 > V S V E W A I D R G L Y S R E Q V E L H E L A G T A I A G D
 25737 TGCCCGCGCGGAGATGGCGCTGCGCGCCGCCCAACAGCGGTCAAGCGTGGGGCGGCTCGCCGACGGAGTTCGACCTGCTGCTCTACGCC
 > L P A P E M A L R A A Q Q A V K R W G G S P T E F D L L L Y A
 25829 AGCACCTGGCACCGGGCCCGACGGCTGGCCGCGCACTCCTATCTCCAGCGGCACCTGGTCGGCGGCGACCTGCTGGCGTTGGAGATCCG
 > S T W H Q G P D G W P P H S Y L Q R H L V G G D L L A L E I R
 25921 GCAGGGCTGCACGGGATGTTACGCGGTTTCGAGCTGGCGCGCAGCCACCTCCAGGCGGTACCCGAGCGCACCGAGCCCTGCTGGTCGCGCG
 > Q G C N G M F S A F E L A A S H L Q A V P E R T S A L L V A
 26013 CCGACAACACGGCACCCCGATGGTCGACCGCTGGCGGATGGGCCCGGCTTCATCGGTGGCGATGCCGGCAGCGCCCTCATCTCACCAAG
 > A D N Y G T P M V D R W R M G P G F I G G D A G S A L I L T K
 26105 CGACCCGGCTTCGCGCGGCTCCGCTCGGTCTGCACCAAGTCGGTCCCGAGGCCGAGCGGTGCACCGGGCGACGAGCCGCTGTTCCCCCC
 > R P G F A R L R S V C T K S V P E A E R L H R G D E P L F P P
 26197 GAGCGTCCTGACCGCGCGGAGCTGAACCTCACCGCCGGATCGACCAACAGTTCGCCGCCCGCAGCCCCGCTCGATCGCCATGGCGGACG
 > S V L T G R E L N F T A R I D Q Q F A A R S P A S I A M A D
 26289 TCGGCGACCACATCGAGGAGGTGCTGGGGCGGCCCTCGCCGAGCGGAGATCGAGTTCGGCGACCTCGCCAGGGTCGCCCTTCATGAACTTT
 > V G D H I E E V V G R A L A E A E I E V G D L A R V A F M N F
 26381 TCCCGGAGATCATGGAGCAGCGCTGCCTGGCCAACTGGGGCCCTGCCCATGAGCCGCTCCACCTTCGACTTCGGTCGCCGGATCGGGCACCTG
 > S R E I M E Q R C L A N W G L P M S R S T F D F G R R I G H C
 26473 CGGGGCGAGCACCCCTTGCTGGCCCTTGAACACCTGGCCAGGACGGGGGGCCCTCGGCCCGCGGATCACCTGCTGACCCCTCGGCACCCGCG
 > G A S D P L L A L E H L A R T T G G L G P G D H L L T L G T A

FIG.11A(23)

26565 CCGGCGTGGTGTCTCGCGGATCGTCCAGGTGATCGAGTCGCCGACGTGGCGGGGAGTGACCCGCTGGACACCTGCGGCGGCGCCGCCCA
 >P G V V V S C A I V Q V I E S P T W R E .
 26656 GCCCAGCAAACGACAGAGGGGATGATTGTGGAAGCAGAGAAGGACCGGTTGCGTCCGGTGGCGTCCGAGGCGGTGCGCGTGGTGGGGA
 >V E A E K D R L R P V A S E A V A V V G
 26746 TCGGCTGCCGGTTCCCGGGCGACGTCAACTCGCCCGACGAGTTCTGGACCTGCTACCGGGGGTGCACACACCGGGACGGTGCCCGGAG
 >I G C R F P G D V N S P D E F W D L L T G G R N T T G T V P E
 26838 GAGCGTGGAGCGGTACCGCGACCTGGGTCCGGGTTTCGAGTCCGGTCCGGTCCGCCACCCGGGGGGCAACTTCTTGCCCGACATCTC
 >E R W S A Y R D L G P A F E S A L R S A T R A G N F L A D I S
 26930 CGGCTTCGACGCGGACTTCTTCGGCATCTCCCGCGCGAGGCCGAGCTGATGGACCCGCGCAGCGGCTCATGTGGAGGTGACCTGGCAGG
 >G F D A D F F G I S P R E A E L M D P Q Q R L M L E V T W Q
 27022 CGCTGGAGGACGCGGGATCCCGCCCGCACCCCTGGCGGCGCACGACGTGGCGTCTTCGCCGGCGTGTGCACCTACGACTACGGCGGCCAC
 >A L E D A G I P R T L A G T D V G V F A G V C T Y D Y G G H
 27114 CAGTTGGAGGACCTGCCGCACATCGACGCTGGACGGGCATCGGCGCCGCCACCTGCGCCGTCGCCAACCGGGTCTCCCACGTCTCGACCT
 >Q L E D L P H I D A W T G I G A A T C A V A N R V S H V L D L
 27206 GCGCGGGCGAGCCTGTGATCGACACCGCTGCTCGGCGTCGCTGGTTCGCTTGCACCTCGCCGCGCAGAGCCTGCGGCTGGCGGAGAGCA
 >R G P S L S I D T A C S A S L V A L H L A A Q S L R L G E S
 27298 CGCTGGCCCTCGCCGGCGGGTCAACCTGATGTCACGCCCGGGCAGTCGATCACCTCGGCTCGGCCGCTGCCCTGGCACCCGACGGGCGC
 >T L A L A G G V N L I V T P G Q S I T L G S A G A L A P D G R
 27390 AGCAAGTCCTTCGACGCCACCGCGACGGCTACGGTCTGTGGCGAGGGGTGCGGCGTCTCTGCTCAAGTGTCTCCGACGCCAGCGGGA
 >S K S F D A T A D G Y G R G E G C G V L V L K L L S D A Q R D
 27482 CGGGGACCGGTGCTGGCCGTGCTCGGGGGCAGCGCCGTCAACCAAGGACGGCCGGACCATGGCACCCTGCGGCCAGGCCCAGG
 >G D R V L A V L R G S A V N Q D G R T N G I M A P C G Q A Q
 27574 AGCACGTGATGTCGCGCCCTGCGCTCGGCGCGGCATCGAGGCGCGCAGCGTCGACTACATCGAGGCGCACGGCACCCCGCTCGGT
 >E H V M V R A L R S A G I E A G S V D Y I E A H G T G T P L G

FIG.11A(24)

27666 GACCCGATGGAGGCCGGCGGATCGGCTCGGTCTACGGGCAGGACCGCCCGGACGAGCCCTGCCTGATCGGTTCCGGTCAAGTCCAACAT
 > D P M E A A A I G S V Y G Q D R P D D E P C L I G S V K S N I
 27758 CGGCCACCTGGAGGGCGCGGCCGCTCGCAGGGCTCATCAAGGCGGTCTCTGGCGCTGAACGGGGCCGAGGTGCCCGCCACACCTGCTGGTCA
 > G H L E G A A G V A G V I K A V L A L N R A E V P A T L L V
 27850 CCGAGGTCAACCCGGACATCGAGTGAAGCGGCTGGGCTGGCCTGGTACCCGCAACCAAGCCCTGGCCGGACCGGGCCGGGGCCGGCCGGC
 > T E V N P D I E W K R L R L R L V T R N Q P W P D R P G P R R
 27942 GCCGGAGTCTCGGCTTCGGCTACGGCGGCACCGTGGCGCACGTGGTGTGAACAGGCCCGCCGGTGCCTGCCGAGCCGGCCCGGGCGCT
 > A G V S G F G Y G G T V A H V V L E Q A P P V A A E P A P A L
 28034 GACCGGCGAGACGTGTTCCCGATCTCCGCGGCTCCGCGCACTCCCTTCGCGAGCGGGCCCGCCCTGGCCGGGATCGTCCCGGATGTCG
 > T G E T L F P I S A G S A H S L R E R A R A L A G I V P D V
 28126 ACCTGCGCGGCTCGGGCACACCTGGCTCGGGCGGTTTCGCACCTGACCCACCGGGCGGTGGCGGTGGCCGGCGGGACGACCTGGTC
 > D L A A L G H T L A R R R S H L T H R A V A V A A G R D D L V
 28218 GCGGCGTTGCGGCGCTCGCCGACACAGGCGGCACGACCGGGTTCGTACCGGAAGCCCGGTGGCGGAGCCGCCCGCACGGTGTGGGTGTT
 > A A F A A L A D D R P H D R V R T G S P V A E P P R T V W V F
 28310 CTCGGGCACGGTGCAGTGGACGGGCATGGGGCGGGAACCTGCTGGCCACGGAGCCGGCCTTCGGGACGCGATCGACCGCATCGAGCAGA
 > S G H G S Q W T G M G R E L L A T E P A F A D A I D R I E Q
 28402 TCTTCTCGACGAGATCGGTTTCTACCCCGCCAGGCGATCCTCGACGGCGACTACGAGCCGTCGACCGGACCCAGACAATGATCTTCGCG
 > I F L D E I G F S P R Q A I L D G D Y E A V D R T Q T M I F A
 28494 ATGCAGCTCGGCTGGCCGAGATGTGGCGAGCGAGGGGAGTCGAGCCGACGCGGTGATCGGCCACTCGGTGGAGAGATCGCCGGCGCGGT
 > M Q L G L A E M W R A R G V E P D A V I G H S V G E I A A A V
 28586 GACCGCGGCATCCTGACCGTGGCGGACGGCGCACGGTCTGATCTGCCGTCTCCCTGCTGCTGCGGAGGTGCGCGGCCAGGGCGCGGATGG
 > T A G I L T V A D G A R L I C R R S L L L R E V A G Q G A M
 28678 CCCTGGTGACGCTGCCCTTCGAGGAGGTGCGGGCCAGGCTGGCCGGCCGCGTCGACGTGGTGGCCGCGATCGCCTCCTCCCGCTCGTCGACC
 > A L V T L P F E E V A A R L A G R V D V V A A I A S S P S S T

FIG.11A(25)

28770 GTGGTCTCCGGCGACCCGGCGCGCTGGACGCGCTGGTCCGCCGAGTGGACCGAGGAGGGCCCTGGGGCTACGCCGGGTGCCTCCGACGTGGC
 > V V S G D P A A L D A L V A E W T E E G L G V R R V A S D V A
 28862 CTTCCACAGCCGCACATGGATCCGCTGCTCGACCGGCTGCGCGCCGCCGCTCGACTTCACCGCCCGCGCACCCCGGGTGCCGATCTACAGCA
 > F H S P H M D P L L D R L R A A V D F T A R A P R V P I Y S
 28954 CGGGCTGGCCGACCCGGGGCCCCGATCACCGCGACGGCGAGTACTGGGCCGCGAATCTGCGCAACCCGGTCCGGCTCGCCGCGAGCGGTG
 > T A L A D P R A P I T A D G E Y W A A N L R N P V R L A A A V
 29046 GCCGCCGCCGTCTCCGACGGACACCGGGCCCTTCATCGAGGTCTCCCGCACCCGGTGGTGACCCACTCGATCCACGAGACGCTGGCCGGGAAG
 > A A A V S D G H R A F I E V S P H P V V T H S I H E T L A G S
 29138 CCTCGACGACGAGGTCTTCGTGGCGGCACCTGCGCGCGGACACCCCGGAGGCGCAGGCCTTCTGTCCAGCCTGGGGGCCGCGCACTGCC
 > L D D E V F V G G T L R R D T P E A Q A F L S S L G A A H C
 29230 ACGGGGTGCGGTGACTGGGGCCGGGTGCATCGTCCGGGCCGTGGTCAACCCTGCCCGGCTACCCCTGGCGGCACCGGAGTCACTGGGCAC
 > H G V A V D W G R V H P S G P L V T L P G Y P W R H R S H W H
 29322 TGGCCGACGCCGCCGCCACGGGCCGGGGCCACGACCCCGCGTGCACACACCCTGCTCGGCGCGGTGCACAACGTGGCGGGCAGCGACGT
 > W P T P A A A T G R G H D P A S H T L L G A V D N V A G S D V
 29414 GCGGGTGTGGCGACCGCACTCGACGACGCCAGCGGCCGTACCCGGGACGCCACGCCCTCAACGGCGTGGAGATCGTTCGGCGGCCGTGC
 > R V W R T A L D D A S R P Y P G S H A L N G V E I V P A A V
 29506 TGGTGGAGACCCTCATGGCTGCCCGCGGGCGGCGGCGGCTGCTGACCGGCTTGTCGATGCGGTACCCGCTGATGACCGCGCGGG
 > L V E T L M A A A G R G D G R P L L T G L S M R Y P L M T A G
 29598 CTGCACGAGGTCCAGGTGGTGGGACGGTGCCGAGGTGGCGTCCCGTCCGTCGACGGGAGGCCGACCCGAGCCGGGACTGGCT
 > L H E V Q V V R D G A E V R L A S R S V D A E A D P S R D W L
 29690 GATCCACACGACGCCAGGTGGCCGACCGCGACGGTGTCTGCCCGCGGGCGGTGGCCGACCCCGACGACCCGATGGAACCGG
 > I H T D A T V A D A D A T V L A A R A L A D P D D H R M E P
 29782 GCGACCCGGGCTCCATCCACCGCGGCTCGCCGAGGTGGGGTGCCGTCGACGGGATTCGACTGGTGGAGGAGCTGCTCTCCGGGTAC
 > G D P G S I H R R L A E V G V P S T G F D W S V E E L L S G Y

FIG.11A(26)

29874 GCGGTGCTCCGCGCGGGTGCGCTCGGCGCGACTCGTCCACCTGGGCGCGGTGCTGGACGCCGTGTCGCTGCGCCCGCGCTTCC
 > G V L R A R V R S A D S S T W A P V L D A V M S V A P A V F P
 29966 CGGCGTGCCGCGAGCTACGCATGGTGTACGTGACGAGGTGCTGCTACCGCGCGAGCCACCGGAGGTGACGCTGATCGAGGTGCGCCCTCG
 > G V P Q L R M V V Y V D E V L L T G E P P E V T L I E V A L
 30058 ACCCAGACCGCGCGACACGGCGAAGCGCTGGTCGCGGATGCTCAGGGCGGGTCTGTGGCCAGCCTTCCCGGGCTGCGCTACCCGGTGATC
 > D P D R P D T A N A L V A D A Q G R V V A S L P G L R Y P V I
 30150 GACCAGCGGTGCCCCGGCGCAGGACAGTTCCGGCGAGGTGGAGGCGGTCTCCTTCGCCGGCCTGTCCGACGAGGAAC TGACGAGCG
 > D Q P V A P A Q D S S G E V E A V S F A G L S D E E L H E R
 30242 GGTGTTGACGAGGTGCGCCGGCAGATCGCCGGGAGATGCGACTCGACGCCGACGACCTGCATCCCCCGCGCGCTGGCCGAGCAGGGCC
 > V F D E V R R Q I A G E M R L D A D L H P R R P L A E Q G
 30334 TCGACTCGGTGATGACGGTGGTATCCGGCGACGCTGGAGAAGCGCACCGGGCGGAGCCTCTCCCCGACCGTCTTCTGGCAGCGGCCACCC
 > L D S V M T V V I R R R L E K R T G R S L S P T V F W Q R P T
 30426 GTCGCGGCCATCGCCGACCACCTGGTGGAGCTGTTGAGCACCCCGCAGGAGTGAGGATCCGCGACGACAGGAGGGCCCGTGC GTTCCGCA
 > V A A I A D H L V E L L S T P Q E .
 30517 CGGGCCCTCCCTGCTGTCGACGGATCTTCAGGTGGGGGTGTCAGCCCGCGCGTGGTCCACCGCAGGGTGCGGGCCCTCCAGGTGGCG
 < . G P R Q D V A P T A A W E L H R
 30608 GCTCTCCGCGAGGGTCTCCTCGGCGTTCGACCCGCGCATGGCGACGCGCAGCATCGGCGCGCCATGACCGAGGTGACGACCGCGA
 < S E R L T E E A N Q E V R R M A V R L M P P A M V S T V V A V
 30700 CCAGCACCATGGTGTATGAGCGGTGTTGAGCACGCCAGCGCGCAGCCCGACCATCGCGATGATCTCCACGGCACCGCGCGTTG
 < L V V I T Y S A T N L V G L R L G V M A I I E V A G R A N
 30792 AGCCCGCGCGAGGGCGACGCCCTCCAGTGGCTCTGCCGGGCCAGCCGTGCACCCAGGTACGCGCGGTGTACTTGCCGAGCACGGCGAG
 < L G A G L A V G E W H S Q R A L R A G L Y A G T Y K G L V A L
 30884 CGCCAGGATCACCGCCCCGCGGAGCACCTCCGGTTCGGCGAGGGCACGCAGATCGACCCGGAGCCCCCGCTGGCCAGGAAGATCGGGG
 < A L I V A G A A L V E P D A L A R L D V R L G A S A L F I P A

FIG.11A(27)

30976 CGAGCAGGACAGCACCCGTGCGCAGCGGTGCCAGCGGGCCGGCTCCCCGTTGCCGGGAAGGCCGATCAGGACACCCGCCACCAGCGCG
 < L V S L V V T R L P A L R A P E G N G P L G I L V G A V L A
 31068 CCGAAGATCGCCTCCAGGGCCAGCGGTGCGCCCCCGCGCGGAAGGCCAGCACGATCACACGGCGACGGCGCTGGCGGGCCCCGCCGTCCGG
 < G F I A E L G L A H A G A A F A L V I V V A V A S A A G G D P
 31160 CTGGCGTTCCGCCAGCGCATGGCGCGCCGGGTACCGGGCCGGCCAGCAGGACGGCCACCGCGAGGTAGGCCACGAGGTAAGCAGGGCGG
 < Q A N A W R M A R R T V P R G V L V A V A L Y A V L Y L L A T
 31252 TCACCACCTGCCCCGGGTGAGGTGCTCACCGCCACCAGAGATGAGCGACAGCAGGAACACGGCCGACGCTCTCCAGCGACGCCGCA
 < V V Q G A T L T S V A V S S I L S L L F W A A A D E L S A A
 31344 GCCAGGATGATCTGCCCCACGTGCGGGTGACAGGGCGCATGTGGTGAGCGTCTTCGCGATCACCGGCACGGCGTGACCGCCATCGCCAC
 < A L I I Q G V D R H L L R M D T L T K A I V P V A S V A M A V
 31436 GCCGACGAACAGCGGAAGACAGTCCGCTCCTGCCCCGGCGCGAGAAGCGCCCGGGGCCAGCAGGCCGGCGGATGCCCAGGCCGAGGG
 < G V F L A F V T R E Q G A A L L A A P A L L G A A I G L G L P
 31528 GCACCGGAGGCCCGCAGGCCACCGCGCGATCGTGCCGGCCCGCGCGGACCGCGCAGGTCAGGTGCAGACCGGCCACGGCGACC
 < V A L G G V A V A G I T G A R R R V L R L D L H L G A V A V
 31620 AGCAGTACGACGCCGAAC TGACCGATGGCGTCGAGCAGGTGGACCTGGTCGGGGTCGGCGGCAGCAGCCACCGTCCGATGTCGGGTGCCAG
 < L L V V G F Q G I A D L L H V Q D P D A P L L W R G I D P A L
 31712 GGCCCCCAGCACCGAGGGCCGAGCAGCACCCGGTCAGCAGCTCACCGACCCAGCCGCGGCGAGCGTTGCGCCACCCGTCCCAGGA
 < A G L V S P G L L V G T L L E G V V A P L G F R Q A V R G L V
 31804 CGACGGCAGCAGCAGCAGGCCACCTGGAGCAGGAACAGCAGTAGCTGGTGGGAGCCACGCGGGGGCACCGCGCGGCCACGATCA
 < V A L L L L L G V Q L L F L L L Q H S G L P P V
 31894 CGGTGTTGTTCTTCGTCGACGCCGGCGGGGCCCGCGGTGGTCAGGCCGCGATCTCGGGCGCAGGTCCACCGGTGCGGCCGAGT
 < A A I E P P L D V P D A S N
 31985 TCATGAAGTCCGAGGGCCCGAGGTGCGGGCGGGGCTTCTCCAGCCCCAGCCCGCGCACCAATCGATGAGGGAGGTGAGTCCCCGGTG
 < M F T R L A R L D A A P K E W G L G A C W D I L S T L E G T

FIG.11A(28)

32077 GCCCGAACCTTGCTCCTCGGGCAGGCTGAGCACCGACATCTCGGCGGCCACTGCACCACGTTGGCCAGGTCCACGTCGAGCCCTCGGC
<A R V K D E E P L S L V S M E A P W Q V V N A L D V D L G E A
32169 CCGGGCGAACTCCAGCAGGTCCGCGAGCCCCAGACGTTGTCCCGTGGGTGCCACCTGGAGCCAGAGTTGACCTCCGAGCGGGCCCGGC
<R A F E L L D R L G W V N D R Q P A V Q L W L N V E S R A R R
32261 GGACGTTCCGATGAAGTCTCCCACTTCGCGCCCTGCCGGATCCGCTCGAACACCTGCCGTAGCCGTGCAGGAGGCCCGATGCCGATG
<V N A I F T E W K A G Q R I R E F V E G Y G D C S A G I G I
32353 CTC TTGAAGTCCGGAACCGGTGGAAGACCGACTCCGGCAACACGGTGAGGTGGAGTTGTAGACGACGTCGACGTTGCCGGCGTTACCCGT
<S K F H R F R D F V S E P L V T L N S N Y V V D V N G A N G T
32445 CTCACCAGCAGGTCGAGCAGGGCGAAGTGGCCCGGTGCATGAACGGTCCCCACCGCGGAAGTACAGCCCGGATGAGGTGGCGTTCT
<E V L L D L L A F H G P Q M F P E G G A F Y L R R I L H A N E
32537 CGCGCAGGTCGCCACAGCTCGTCGTCCCGTAGGCGTCGATACCGCGGACGACAGGCCGGCCGCTTCTTGGCGCCCGAGCCGAG
<R L T Q W L E D D R Y A D I V A S S W A P R K K A G W G S
32629 CTGACCGGTACGCGCACATCAGCACCGCAGGTTGCAGGTGTTGCCGAACCGGATGTCGAGGAAGAACGGGAAGTCCTCGACGGTGCCGTC
<S V P Y A C M V C R L N C T N G F R I D L F F P F D E V T G D
32721 GGGCGCGTGGGGCGCCAGCCGGTCGGGTCCGGATGTCCGGAACCGCTGGTTGATCTCCTGCCGTACGACAGCGCGCGTGGTCCT
<P A T R A A L R D P D A I D R F R Q N I E Q R Y S L A G H D E
32813 CGCGGTGTAGCAGTAGGAGCAGGCGTCACCCGCTCCCGGCCAGCATCGCCAGCGGGTCGGCGCATGTTGGGGCTGTTGAAGGCGTC
<R H Y C Y S C A D V R E G A L M A L R T R M
32904 CGCCAGGCCCATACCCGGCCGGGTTGTCGCGCGGTAGCGGGACCGCGGAGCAGCCGACGGCGTCGTCGTTGAGCAGGAACTCGGGCT
32996 CCTCCTCCTGCTGTACAGCTTGTGTGATCATCGAGTCGTCCACGACGACCCCGGTAGACACCGTCGATGGACCGCAGAGATGGATC
33088 CAGGGCAGCACACATGGTCCGGACCGGGCTTCCGGGTCAGTCATGAAGTTGATCACCTCGGTGGTGGGGCGGTGTCATCCCGGTCG
< . G P R
33179 GCCGACCGTCTCGACCCGGGCGAGCGGAAGATCAACCGGGTGCCGCTGGCCAGCATCTCCGCCCTCCCGGGCGACGATCTCGTCCCGGAAGT
<G V T E V R P L P F I L R T G S A L M E A E R A V I E D R F H

FIG.11A(29)

33271 GCCAGGGCAGGACGAGTAGTCCGGGGGGCCCGCGGACCTCCTGCTCGCTGATGATTTTCGATGTCGTGCCGAGGGTGCGGGCGGCC
< W P L V L Y D P R A A R S E Q E S I I E I D T G L T R A G
33363 ACCTTGTCGGATTGCGCTCCGCGGGGTACCGGATGAGCTCGGGTCTATGCCGCAGAACTGCAGGAGGGTGTTGCCCTTCGTGACGGCGCC
<V K D P N R E A A Y R I L E R D I G C F Q L L T N G K T S A G
33455 GTAGACGTGCACCGTCGGGCCCTGGCCCCGAGCTCGGCGAGCAGGGCGCTCACCTGTCACGGTGCTGGCGCACCTGCTCGGCGAAGCGCT
<Y V H V T R G Q G R L E R L L A S V E D R H Q R V Q E A F R Q
33547 GGTACGGGGCGTCGCGTCCAGCCCCAGCGCCAGCTCCCGGTGCGGAGTGCCTTGACCGAACCGTCGGCCCCGCGCCACCTCACCGGCC
< Y P A D G D L G L A L E R D A L A K V S G D A R G G V E G A
33639 CGGGTGACCACGACGATCGAGCCCGTTACCCCGTTGAGGTGGCACGGACGATCTCCAGGCCCGCGCCAGAAATGCGGCTCAG
<R T V V C C I S G G N V G N L S A R V I E L G A A G L I R S L
33731 CGTGGCCAGCGAGTAGGACAGGTGCTCGTGGCAGATGCTGTAGCCGGCGATCTCCAGCATCGCCGGCAGGTAGGCGACCTCGACCA
<T A L S Y Y S L H E H C I S D Y G A I E L M A P L Y A V E V V
33823 CCCAGACCCCGCGGGCGAGCAGCGCTCGACCTGACGGCGAACTCCACCGGTCTCTGACGTGCTAGAACATCGCGATCGAGGTGACC
< W V G G P A L L A E V Q R A F E V P D E V D Y F M A I S T V
33915 AGGTGGAAGTCCCCGCGTGCGGACCAGCTCGGGGTGGGAAGAAGTCGCGGATCAGATTGAAGTCGTGGGCGCGTCGTGCGGGCGCT
<L D F S G A H P V L E P S P F F D R I L N F D D P A D D A A S
34007 GGAGGGTCGATGCCCCACCGCTGCGGTGCGGTGAGTTGCCAGAGGGTGCCGTGCTTGCAGCCGATGTCGAGCACCTTGCCGGGGCGCT
<S P D I G W R Q A D T L N G L L T G D N C G I D L V K G P R E
34009 CCCCCAACCTCGACCGCGCTCCACGACGTGCGCGAGATGCCGGCGCATCGTGTGTTGATCCGCGAGCGGTACCAAGTGTCTGTAG
< G L V E V A A D V V D A L H R R M T D N I R S R Y W Y T D Y
34191 AGCAGCCACCCGCGAGGGTGTCGCGCAACTGCACCAAGGCCCGCACGGGTACCCGCGTCGCGTTCGCGCACCCGGTCAGTCCAGGGGGAA
<L L G G P L T H R L Q V L G C P D G G D R E A C R T L E L P F
34283 GCGCACCTGGGCGGTCCGACACGCGGGCTTACGAAGCTGCCCTGTAGTACTGGCACCGAGGTGAGGACCGTACGAGGGTCCCGC
<R V R P P D S V G P K V F S G Q L Y Q A G L D L V T R L T G G

FIG.11A(30)

34375 CACACACCCGGCAGGTGGTCCGCTCGACCACCTCCGACGCCAACTCCTCGCCGGCCGCCCAACTGGCTCAGGTCAGGTCCCTCCTCGT
< C V R C T T R E V V < R T R R T
34464 CTCGTGCCGGTGTGCGGGACGAGGCCGCCCGTCGTGCGGTTTGTGGCGACACGACGAGTGTCCAGATAGAAAGGCTGGTCGGGGCCCTCGC
< E H R H A P G P A G D H P K S A V L L I D L Y F P Q D P G E S
34556 TCGCGCCGAGATGCCGGAACGCCCGGTGAGGTACTCGTCGAGCGCGGGGCCGAGCCGGTCCACGACCAGGGCCGCGCAGGGCCAGA
< R G L H R G A R D L Y E D L A R P R L R D V L W L A R L A L
34648 CCCACCGGGCCGCGGACGGCCAGCCGTGCTCGGGCCGTACCAGCGCAGCAGCAACAGGCCGCGGGCCCGCAGGTACGTTGACGGT
< G V P G G S P W G H E R G Y W E L L L L L G R P G C T L K V T
34740 GCGGTGACGGTGAAGCCGGCCCACTCGGCCTGGCGGGCCAGCCCGTCGGCGGTCCACCGCCACAGGTCTTGGCCGCCGTGCTCCTCCCACA
< R D V T F G A W E A Q R A L G D A T W R W L D Q G G H E E W V
34832 CCCC GTGGTGGAGAGCACCCCGTCGAACGTCCCGTCCGGCACCGGGCAGCAGCGGTACGCCTCCCGCAGGTACGCGTCCGCGTCCGAGACGTGTTCCGAGC
< G H T S L V L R G G P R L L R Y A E R L Y A D A D S V H E L
34924 ACCTGGGTGGAGAGCACCCCGTCGAACGTCCCGTCCGGCACCGGGCAGCGCCCGTCGCCGTTCGAGGGCGTGGTCGGCCGGCAGGACTCACC
< V Q T S L V G D F T G D P V P C R G D R D L A H D A P L S E G
35016 GCCCGGGATGTGGCGGTCTGCAACTCGGCGGAGCGGAACAGGCCCGGTATGGCGAGGTGCCCGCGCGGTAGTCGAGCCAGACTCCCGTGG
< G P I D A T Q L E A S R F L G R Y P S T G A G Y D L W V G T A
35108 CGTCCCGGACCGCTCCGCCAGCGGTCCGCGAGGTCCAGGAAGTGGCGGTATGCCAGTCCCGGGCCGGGGCTCGATCCGCTCCCGGAAC
< D R V A E A L A D R L D L F H A Y A W D G P R P E I R E R F
35200 CGTTCGGCCATCACCTCGTCCAGCAGCGGGCGGTGGGGCGGTGCCGGCACCGGTTCAGCAGGGGACCAAGCCCGGGTACGCGCGGCAGC
< R E A M
35290 AGGTCACCAACGCCAGTACTCCTCGTGGGGTACCGCATGGTGGTCCGGCTCCGGCAGGCCCTCCAGCGCCGACGACGCGGGGGCCG
< W R W Y E E H P Y R M T T P E P L G E W R R L S A A P R
35381 GTACTCGAAGGGTGTCCCGCGGTGCTCCGGTCCGCCCGCCCGCTGCCAGGAGAGCAGCACCTGCTGTGAGCCCGATGTACT
< Y E F P Q E G A H E P A A R R Q A L C S L L V Q Q K L G I Y E

FIG.11A(31)

35473 CCGGCACGTGCGGGCCGAGGTCCAGCTCGACCTCGGGGGCCGGTACTCGAAGTAGATGACCCGGCGCCGCTTGCCGGTACCCGCCGGCGG
< P V H P G L D L E V E A P R Y E G Y I V R R K G T V A P A
35565 GCGTGCAGCATCAGGATGTTGTGCAGCATCAGTCGCCCGGGTTCATACCCGCCGGCACCCCGCGGTGGTGTCCACTCGGTGGCGTTTCAT
< A H L M L I N H L M V D G P N M V A P V A G T T D W E T A N M
35657 CCGGGTGGTCTCGTTCGCCCGGTGGTGTCCAGTAGTTCGACTGCGGGATGCACAGACGCAGTTGTCTCCGGGGCCGGGTCAAGGT
< R T T T E N A R D T D W Y N S Q P I C W V C N D E P A P D L Y
35749 AGATGCCGACGTGATCACCCGGCCCGCGGTGATGCCAGCCGGTTCCTCCGGGTAGAGCCCGCGTGCGGTGCCAGGGCAGCCGGGGC
< I G V D I V R G A G T I G V A N E P Y L G G D R H W P L R P
35841 GCCCCCGCCTCGGTCTTGAAGACCATGCTGTCCAGGTGGGGATGAGGTGGGGCCGACCAAGTCTCTCCATGCCCGCAGCAGCGGGGTG
< A G A E T K F V M S D W T P I L N P G V L D E M A R L L L P H
35933 GCCGGGAGCCGGGCGACACCGGGGACTTGTGACCACGTACTCGATCCGCACCGCGCGCGTCCGGTCTGTCGGTTCAGCGTCCAGA
< G A L R A V V P S K D V V Y E I R V P A A D P E H P E L T W I
36025 TGGTGTGGTTCATGTCGGGTGCGCAGGCTTCGTGATCAGTCTGTCGGCCCGCGCTGCACGGACCGAGTCTGTCGGGTCCAGCAGC
< T D T M T R T R W A E D I L E D A A A Q V S R L E D P D L L
36117 CCGCGCAGGATCAGCGGCCCTGCCGGCGGAAGGGGTCAAGTGTCCGGAAGCAGCCCGGTCTCGTGGATGTGGCACTCGGGGACGGCCTG
< G R L I L A G Q R R F A T L H E P L L G T E H I H C E P V A Q
36209 CTCGGTGGGACGTCCACAGTCGCGTTCATGGTTCGGTTCCTTCTGCCAGGCGGACGGTTCGTGCTGCCCGGAGCCGCCGGCGGCCG
< E T R V D V T A S M
< . P E T G K Q W A S P E H Q G S G G A P G P
36300 GGCTCGGTGGTGACGAAGTACCAGTGTCTCCGCGAGCGGTCCGGCGAACCCCGCGGTCCAGCGCCGGTGCCTGCCGGCGGCCGCGG
< S P R D A V F Y W H E R L A D A F G A R D L A P Q G A R R G
36392 GGCAGGGTACGAGTCTGTAACCCAGTCTGGTCAACGACGCGCCACAGGTGCGCGCTGGTGGTGGCGTACTCCCGCATGGCGTGGTCCGC
< P L T R L E Y G L E T V L L A W L D A S T T G Y E R M A H D G
36484 GCCGTGCTCGAAGACGATACCGGCGCGCGGAGCAGCTCCACGGCACCCGCGCAGGGCGAGCACCTCGCCGCCCTCGGTGTCCACCT
< G H E F V I V P R W R R L L E V A G R L A L V E G G E T D V K

FIG.11A(32)

36576 TGACCAGGTCGATCCGGCGGTACCGGGGAGCACGTCGTCCAGGGGACGGTGTGACCGTCAGCTCCCGCAGGGTCTCGTCCGGGCGGTGCG
 < V L D I R R D G P L V D D L R V T D V T L E R L T E D P R D
 36668 TAGGGACCGCGGCGAGCCCGCTGTAGCCGGGGTTGGAGACCACGTGGACGAAGCTGTCCCGGCCGGTGGCTCGGCGGCGGCGGCGGCGCAC
 < Y P R R R L G S Y G P N S V V H V F S D R G T R E A A A A V
 36760 CACCGTCACGCCGGGAAGTCCGGCGCAGCCCTCGCGGTACGACGGCAGCGCCTCGACGGCCACGTGCCGGCCACGGGGGGCGACCCGCA
 < V T V G P F D R R L G E A Y S P L A E V A V H R G R P A V R L
 36852 GCAGGTGACGCAGGATGTGCGCGGCGGCCCCGATGTCCACGGTGTGGCGTCCGGTTCGCAGATCTGCTCGATCAGCGCCACGGTGAGC
 < L H R L I D G A G A G I D V T N A D P E C I Q E I L A V T L
 36944 TGGTCGTACCACTGTTTCATCGACAGCGCGCGGCTCGTCCGTCCGGAAAGCTCAGTGGACATCTGTCAGGCTCCTCGGTCCGGCACGCC
 < . H V D D R E E T R C A
 < Q D Y W D N M
 37035 GGTCCGGCCCCGAGCCGACCGCGGGCGGTACGGACAGGAGTTCAGCTCCCGCAGCTCGATCTCGACAGCTCCAGGCCGGGCGCGG
 < P G A G S G V A P A T R V L L E L E R L E I E S L E L G A A R
 37127 GACGTTCTCTCGACGACTCCGGGCGACTGAGCGCGGAACACCGGCACCACCCCGCGGTGGTGCAGCGCCAGGCCAGTGCACCTGCG
 < V N E E V V G P S Q A G F V P V G A P H H L A W A L A V Q A
 37219 CGACGGTGTGCCCCACGCTCGGCGGCGAAGCGCGGAGGCCGTGACCACTCGAGCAGTTGGGCGTAGTCTCACCCCGGAAGCGTGCGAG
 < V T H G R E A A F A A L G D V D L L Q A Y D E G R F A H S
 37311 TAGGCCCCCAGTCTCGGGGGCGAATGCCTGGTCGGGTGCAGCGCGGTGAGCAGCCCGTGGCGGAGCGCGGAGCCCGCCAGCACCCC
 < Y A R W D E P A F A Q D R H L A G T L L G H A L A S G G L V G
 37403 GACGCGGCGCTCTGGCAGCGGGGCGAGCACCTCTTCGCGCACCACTCGGTGAGCAGGTTGAACGGCACCTGGACGACGTCCAGCAGCCCGG
 < V G A E Q C R P L V E K E A G R D L L N F P V Q V V D L L G T
 37495 TCGGCACCACTCGGCCAGGTGCCCCCGCTACGTTGGCGAAGCCGACATGGCGGGCCAGGCCCTCGCGCACCAACCCCGCCAGCACCTCG
 < P V L E A L D G A T V N A F G V H R A L G E R V F G A L V E
 37587 GCGGTCTCCGCGAGCGGACGGTCGGGTCCGGCCAGTGACGGAGTACACGTGACGTGCTCCGTGCCGAGCTGACGCAGGCTGGCCAGCAG
 < A T E A L P V T P D P W H V S Y V D V H D T G L Q R L S A L L

FIG.11A(33)

37679 CTCGTCCCGAGGAACGCGGGTTCGTGTTACGCACCGTCCGTCCGGCGGGTCGAGCTTGCCGTGCACGCCGGGCGGGTCTCCAGCC
 < E D R L F A P D S N R V T R G P P D L K H R R V G P R T E L G
 37771 CGCCGGCGGTGGCGATCAGGATCTGTCCCGGTGCGGGGCAACAGGTGCGGCCAGCCCGGGCAAGGGCGCCTCGGGGCCCCCGCGCGCG
 < G A T A I V I E D R H A P L L D A L G R A L A A E A A G G G
 37863 TACGCCGGGAGGTGTCGAAAAGGTGACGCCAGGTGCAAGGCCCGGGACGGCTGCACGCCTGGTTCGATCCGCCGGCCCCACTGGCC
 < Y A R S T D F L T V G L D F A R R V A Q A G P E I R R G W Q G
 37955 GCCGAGCCCCAGGTGCCAGGCCGAGCGCCGAGACAGCGGCCCGCTCACCGATGCAGCGTGCAGCGTCCCGCACGGCGTCTCCCGCCCCGGTG
 < G L A W T G L G L A S V L P G R E G I C R Q R V
 38046 CCCCACCCAGCCCGTCCGCCGGCGTACGCCCGCGGCTCCCCGTCGTGGCAGCGTCAGGAACACCAGCCGTCGTGATTGATCATCT
 < . A A P E G D S R L T L F V V G D H N I M K
 38137 TGTGGTGACGGCGTCAGCCCGGCTCGCGGGGATGCGCGTCACTCACTCCACGCCGTGCCAGTTCAGGAACCCCTTGAAC TCCACGGGG
 < D T V P T L G A E A A I G T M L E V G H W N L F G K F E V P
 38229 TTCGCGTCCGGTACCGCTCGGCGTAGGTGTGGAAGAAGCCGCGGTGTTGTGCGCGAGGTCCAGGAAGTTGAAGCAGAACAGCCCGCGGG
 < N A D R Y R E A Y T H F F G R T N D G L D L F N F C F L G G P
 38321 CCGCAGGATCCGCCGATCTGACGGAAGTAGAGGAAGACCTCGAAGACGTTGAGGTGATGAACACGTTCAGGGAGAACCCGGCGTCGAACG
 < R L I R R I Q R F Y L F V E F V N L H I F V N L S F G A D F A
 38413 CGGCGGTCCGAGCTTCTCCAGGAAGTCTTCGATGTGGTAGGAGACGTTCTCCGGCCCTCGCAGGTGGCGCGCCTTGTCTGAGG
 < A T P L K E L F D N E I H H Y S V N E R G E C T A R A K D L
 38505 AAGGATCGGTGACGTCCGGCGCAGAGCACGGCGGCACCCGGTCGGCGAGCCCGGCCCATGATGCCCTCGCCGCTGCCGATCTCGAAGAT
 < F S R S V D A C L V A R V R D A L G A A M
 38597 CTCGATTCCGGGCCGAGCCGAGCTGCTCGACGACCAGGGCGACCTTGTGCACACGCTCTGGAGGTACTCTCGCGCGGTGGTAGCCGG
 38689 CGAGCTGCATCTGCATCTCTCCGGGTGTTCCACTCCAGACGTAAGTTGAGGTGCGCGGTGCTCCGGAGCGGACAGCCCCGGGGGGGTCC
 38781 TCGCGCGCGCGTGCCTGCTTCGGTGTTCATCGGACCTCAGTCCGGGTCTTGTGCGGTCTGCGGGGACAAC TGGCGGGCGGTGCG
 38873 GAAAACTGGGCGGGCGGTGTACGGACGCGGGGGAAC TCGCGACGTCCTCGGGGTTCAGCGCGCGGTGTGCGCCAGCCGGGCCAGGAG
 < . P R R A F E A V D E P S L A G T D A L R A L L

FIG.11A(34)

38964 TTCGGCCACCTGGACGGCGGTGGTGACGGACTCCCGCATCCGCTGCGCCGCCACCCGGAATCGGTGGTCTAGAGGACGGAGC
 <E A V Q V A T P G T T V S E R M R Q A A V R F R H D Y L V S G
 39056 CGAGGGCCTCGTCGACCTCCTCGGGGACGCCTTCAGGCGGGCAGCGTCTTCGTCGGCCCTGCGGGTCGAGCCGCCCGTAGATCAGG
 <L A E D V E E R S A K L G P L T K T A G Q P D L R R G Y I L
 39148 GCGTCGTAGTTGAGCGCCAGCACAACCTGCGGCACGCCCATGGCAGCCCCGTTTCATGTAGCAGTTGGCGCTGCCGTGGTGCACCAAGTC
 <A D Y N L A L S L Q P V G M A L G N M Y C N A S G H V L L D
 39240 GCAGTCGGGAGGATGAGCTCCAGCGGGCAGTTGCTGAGCACCCGCACGTTGCGGGCAGCGGCCCCAGCCCTCCACCTCGGAGGAGGCGG
 <C D P L I L E L P C N S L V R V N P P L A G L G E V E S S A A
 39332 CGGTGATCAGCACCTCCACGCCCCGCTGGGCGGCGGCTCGACGGGTGCCGCGAGCGCGGCACCTGCGCGCCGAACACGCCCGTGGCGGAG
 <T I V V E V G R Q A A A D V A H R L A P V Q A G F V G T A S
 39424 TTGCCCCACACGACGACCCGCTTGCCCCGCGCGGACCGAGCAGCGGGTCCACGTCTCTGGGAGCGGTTGTAGGGCTGGTAGCGGAT
 <N G W V V C V R K G R P G L L W P D V D Q S G N Y P Q Y R I
 39516 CGGGATCCGCAGCGCTGCCCATCGCGGGATCGCCACGTGCGGCGACGGGTGATGGCGTACCGGATCTGGTCCGGCTCCACTCGACGC
 <P I R L A D G M P P I A V D P S P D I A Y R I Q H R S W E V G
 39608 CGTACTTGGGAACTCGGTCACCGGGTGGCGGAGACGAGTCGAGCCGGGCTCGGTCTCGATGGTGCCGATGAACCCGGCGAGAAGTAG
 <Y K R F E T V P D G S V L D L G P E T E I T G I F G P S F Y
 39700 ACGCTGGGGATGGTGCAGCTCGGCGACGAGCGGCCCTCCACGGCCATGATGCTGGACCACCGAGTCGGGCCGGTAGTGGGCGGCGTA
 <V S P I H H L E A V L A G E V A M I D H V V L D P R Y H A A Y
 39792 GTCGACCGGTTGCTAGCTGCGCTGGACCGGTTGACCGTGCGCTCCAGTAGTCGGCGAGCAGGTGCGTGTGGAAGTCGGCGAGCGAGT
 <D V A N D Y S R Q V A T V T R K W Y D A L L D T D F D A L S D
 39884 CCATCGGCCGCGGTTCAAGCGCAGCGGTTGCTCCACCATGTGCTCGGGGTGTAGAGGGCCTGGACGTAGAAGCCAGCGCGG
 <M P R G T F P N L P L P Q E V M H Q P T Y L A Q V Y F G L R
 39976 GCGCTCTCCATCATGTGCGGTCCGTGAGCACCGAGCGGGCATCATGCCCGCGCGCCACGCCCGGACCTGGGACGGCGAACAGGCGAC
 <A S E M M D P G D L V S V P M M G A A A V G R V Q S P S C A V

FIG.11A(35)

40068 CTTGACGTCGTGGCCGGCCCGCAGCGCCAGGCCAGCGGCACCATGCACATGTAGTCCCGGCCAGTTGGACACGGTGAACAGAACCT
 <K V D H G A A R L A W A L P V M C M Y H G A W N S V T F L V K
 40160 TCATCGCAGCCTCTCTGTGGCCTGCCGAGGGGAGGTTGGGGTCCGGGCCGACGGTCAGGAGGTCAAGACCGCAACTCCCGCGCGGGA
 < M < . S T L V P L E R A P
 40250 TCGGGGAACCTCGATCAGTGGTGGCCGCCCACTGGTCGGAGGGGTTCCGGCCCGAGCCGTGCACCGCTACGTCGTGGACGATGAAGTC
 <D A F E I V I T R R W Q D S P N P G S G H V L R V D H V I F D
 40342 CCCCTCCTGCGAGGGGACCGCACCCGGCCCCGGGTCCGCGCAGGCCGTGACGTGGCGTCTCGGGCAGCAGGTGGGAGCCCGGGCACGC
 <G E Q S P V P V R P G A D R V A T V D A D D P L L H S G P V G
 40434 CCTCCAGACAGCGTTCTCCGGCCCGCGGTGTCCAGGCAGATGCTGATGTTGCAGACCGCGTGGGGGGGACGTTGACCCGGTCCCGGTGC
 < E L C G N E P G A T D L C I S I N C V A H P P V N V R D R H
 40526 CACGGCACGCCGCCCGCAGTGGTCTCTTGAGCACCAACGGAAGGGGTGGGCACGACCGGGGTGCCGAGGACGTGGCGGCCACCGC
 <W P V G A A R L P E K L V L A F A T P V V P T G L V D A A V A
 40618 GCGGATCTCCGGCGGTGCAGCAACTGCCCCTGCGGCAGTCCTGCTTTTCAGGTTGTGGATCCGGTACAGCACCGGCTCCGCGCCCTCGA
 <A I E P R H L L E G Q P W D Q K E L N H I R Y L V P E A G E V
 40710 CCTCGTAGTCCAGTAGTCGGCGTTGGCCCGCGCGGACCGGGAACCGGTGCATCAGGCTTACCGCGCCGCGCTTGAGCTGGGCCAGCACC
 < E Y N W Y D A N A R A P G A F R D I L S V A G A K L Q A L V
 40802 TCGGGGTCGAGCACCGCCGACGTGCGCGATCCCGTGGGGAACCGGTGGCCACGGCTCGCGCTCCCGCGACATGGTGGTCAATCG
 <E P D L V P G V H A I G D S R F R S A V A E R E R S M T T M
 < . R
 40893 GAGGCTACCCCTTCGGTCGGTCGGCGGTGCCGGTGGGGGGCCGACGGCGATGATGTGCACACCTCCGGCGACCGGCGCTCGTGCAGC
 <L S V G E T P R R T G T R R G V A I I D C V E P S R R E H L
 40984 ACCTCCACCTCGGCGAAGCCGGGTTGTGAGGGGGGGAACAGGGACTCCCGGTGAGCCAGCGACGTGACGCTGAGCCCCCGGGCCTG
 <V E V E A F G A N H L A A F L S E R D L W R V D V S L G R A Q
 41076 CGGCTCGGGGTGCTCCTCGCGGACCTGCTTGACCGGTGTAGCCGTGATCGGTTGCAGGTGCGCCACGCTCCCCAGTAGTGGTGGAGAGGT
 <P E P H E E R V Q K V T Y G D I P Q L D G V G G W Y H T S L Y

FIG.11A(36)

41168 AGATTCCCGCGGACGCCGGATGTCTTCAGCAGGGTCCACGGCTCACGCACGTGGTAGACGAGGCCCGCAGAGGACGGCGTCGAAC
 < I G A A V G A I D K L L T W P E R V H Y L L G A C L V A D F
 41260 TCGCCAGCTCGGTGAAGTCGATCCGCTCCAGCTCGGCGACGGCAGCTCCACGTTGGTGTGACCTTGACCTCCATCACCAGCTCCGCGCG
 < E G L E T F D I R E V D A V R L E V N T I G N V E M V L E A R
 41352 GCGCAGTTCTCCGACGGCCCTCCAGGGCAAGCACCGTGTGCCGGGTGCCGGCGAGGGCAAGCGTGTCCGCGCCCTCCAGTGGCGCGGA
 < R L N E P R G E L A L V T T G P H R A L A L T D A G E L A G L
 41444 GTTCGAGGATCCGCGCGGTCTGGGAACGACCCGAAGAATTTCGGGGCCGGTCTGGCCGGGACTGGCTCAGCAGATAACCGTGTCTGGGAG
 < E L I R R A D P F A G F F K A A R D A P S Q S L L Y G H Q S
 41536 CCCTCGGCGTAACGCACTCCGTCTGTCTGAATCCATTCAACCACGGCTCGAGCGCGGCGACGCGGCGACGAATCTCTTCACGGTCCCATGG
 < G E A Y R V G D H E F G N V
 41627 GATCAAGCCTAGCGATGCCATTGCGGTTGCGGACTAGTGTTCATCATATTACGGGCTCGCCGTGCTGAGCCTTTCTGTTGACCAGCCG
 < . R S A T S L R E N V L R
 41718 GGCCCATTCGGGAATCCGGTCCCGCGGATCTCGATATCGAAGGACGACTGGAGTTCGCGCGGCCGGCGTGGCGCGCCACCTGGCGGTGC
 < A W E P I R D G G I E I D F S S Q L E A P G A D A A W R A T R
 41810 GGGCCAGTCCCTCGGCCAGCGGGGTGTCCGTCCAGTCGCCGAAGACCGATCGGGCCAGCTCCGTGCGGGTGTACGCGGTTGCACTCGTCC
 < A L G E A L P T D T W D G F V S R A L E T A T Y A T R V E D
 41902 CGCGACGGCAGGTGGGCGATCGGATGCTCCGGCACGCGCGCGCCGACCGTACCGCTGGGCCAGCTCCAGCACGGTGTGGTGTCTCGACGA
 < R S P L H A I P H E P V G A A S R V A Q A L E L V T N T S S
 41994 GCCCAGTTGAATGCCCGCCCCACGCGGCTCGGTCTCGGCGGCGCGGTGACCCAGTTCAACCACGTCAACGACGTACGTGAACGCGCGGA
 < G V N F A R G W A A E T E A A R S V V N V D G V Y T F A R V
 42086 CCTGGCCCGCTGCCGTACACGGTATCGGCTCGCCTCGCAGGATCTGTTGAAGAAGATGGCGACCGGTTGCGGTACGGTCCCGCATG
 < Q G G D G Y V T I P E G R L I Q N F I A V A N R Y P D R M
 42178 TTCTGCCACTCGCCGTAGACGTTGTGATGCGGAAGGCGGTGAAGGCGAGCCCTGGTCCGCATCGTCACCTCCAGCTCGCGCTCGACCCAG
 < N Q W E G Y V N H M R F A T F P L G Q T R M T V E L E R E V L

FIG.11A(37)

42270 GTACTTGGCCAGGCCGTAGCTGTCCGGGGACGGGGACGCGGACCTCGCGCATCGGGCTCTCGCCGTGGCCGTAGACCGCCACGGAGGAGG
 <Y K A L G Y S D A P V P V V S E R M P T E G H G Y V A V S S A
 42362 CGAAACAGAAGAACCGCACGCCGGTACGACGCGCGTTGATCAGATTTATGCTGCCCATCACATTGGTCCGTAGTTGAGCTGCTTCACC
 <F C F F R V G T R L S A N I L N I S G M V N T G Y N L Q K V
 42454 GAATGGCTGATCGCCTCCGCCGGAAGCGGAAAGTGAAGACCCGCTCGAATCGGTTCTCGCGAACAGTGAATCGACGAAGTCCACGTC
 <S H S I A E A F A F A F H F V R E F R N E A F L S D V F D V D
 42546 GGTCACCGAACGACGGCCAGGTCCACCCCGCGGAACCCGCTGCCGGCTGCCCGCTGAGGTCTCAGAACGGTGACCCGGTGCCCAT
 <T V S G V A L D V G A P V R Q R S G G S L D L V T V R H G N
 42638 TCCTGACCAATGACTCCACCAGGTGCGAGCCGATGAATCCGGCACCCAGTCACGACACGAACCATCCGGGGCTCCTTCGTCAATA
 <R V L S E V L H S G I F G A G G T V L C R V M
 42728 GATCCGGAAGGGTTGACCGAGCGGGCGATCTGCGGGCGGCCCTTCGTCGGCGAACACCGACCCCGAGAGAAAGCTTCGCCTCAGGGCAC
 <. P V
 42819 CGGCGACCGGTGGCCTGCTTCTCAGCGGCTCCACCAGTCCCGGTGCGTCCGGTACCACTGATCGTCTCGCCAGGCCGTGCGGGAAGG
 <P S R D A Q K K L P E W D R H T R Y W D I T E A L G D A F A
 42911 CGACCTCGGGCCGGTAGCCGAGCGCCCGAGTTTCGGTCCGTACGAGTAGCGGGCGTGTGGCCCTTGCGGTCCGGCACCCGCTCGACC
 <V E P R Y G L A R L K A D T L S Y R R D H G K R D P V R E V
 43003 CGGTCCACCCGGCCCCAAGGCGTCCAGCAGCCCGGTCCAGTCCATGTTGGACAGCTCAGCCGTGCCGGCGATGTGGTAGACCTCGCC
 <R D W G A G L A D L L R G T L E M N S L E A T G A I H Y V E G
 43095 GGGGACACCGGGTCGACGACGGTCTGGATGCCCGGCAGTGGTCCGTACGTGGATCCAGTCGCGGACGTTCCCGCCGTGCGCGTACAGCG
 <P V G R D V V T Q I G R C H D T V H I W D R V N G G D G Y L P
 43187 GCACCCGTGCCCGTTCAACAGCTCGGTGACGAACAGCGGGATCAGCTTCTCCGGAACCTGGTACGGCCCGTAGTTGTTGCCGACCCGGGTG
 <V R R G N L L E T V F L P I L K E P F Q Y P G Y N N G C R T
 43279 AGGACAGCGCAGCCGTGGGTGCGGGGTAGGCCAGGGCGATCAGGTCCCCCGCGCCCTTCGCCCGCCGCTACGGGAGTTCGGCGGCCAG
 <L C V P L G H T R A Y A L A I L D G G A K A A A Y P S N P A L

FIG.11A(38)

43371 GGGGGTGTCTCGGGCCAGGAACCCCTCGTCGATGCTGCCGTAGACCTCGTGGTGGAGACCTGGACCACCCGGGCGACCCCGGCGTCGAGAC
< P T D E A W S G E D I S G Y V E D T S V Q V V R A V G A D L C
43463 ACGCCTGCATAGCGTCTGGACGCCCTGCACGTTGGTGGGAGCAACTCCGCCGAGTCGGCGATGGACCGGTGACGTCGACTCGGGCGGCG
< A Q M L T Q V G Q V N T R V F E A S D A I S R D V H S E A A
43555 AAGTTGACCACCACGTCGTGCCCCGGGCGAGCACCTCGGCCAGCAGCGCCGTGTGCGAGACGTCGCCCTGGACGAAGGTGATCCGGTCCCTGGAC
< F N V V V D H G P L V E A L L A T D C V D G Q V F T I R D Q V
43647 CGGTTGAGGTTGGCGAGGTTGCCCGCGTACGTACGTTGTCCAGCACCGTCACCCGGGCGCTGGCCGTGTGGGGTAGGCACCGGTGGCCA
< P E L N A L N G A Y T L K D L V T V R A Q A T D P Y A G T A L
43739 GGTGCGGCGACGTACTGCGAGCCGATGAACCGGACCGCCGGTGACCAAGGACGCGACATCAGACCCCGGACTTCGCTGTGAT
< D R V Y Q S G I F G A G G T V L V R R M
< . V G V R V E S H D
43828 CGCCGAGGACGAACCGTTCGTCCTTGGGACCCGGGGCCGGGGACCAACCCGGCGCTCCCGCGCATCATCGAGAACTCGATCGGCGCGATG
< G L V F R H T K P V R P G P V V R A E R G I M S F E I R G I
43920 CCCTCGATGAGGCACCGCGCAGCAGCATGGAGTGTGATCTCGGTCTCCAGCAGGTCAGTCGCAGTCGATCGAGGTGTACGGGCGGAG
< G E I Y A G R L V I S H E I E T E L L T C D C D I S T Y P G L
44012 GTAGGAGTTGCGGATGATCGAGCCGGCTCCGACCACCAACCGGGCCGACGATCCGGGAGCCGCTGACGTGCGGCCCGCGCTGATCACCACCG
< Y S N R I I S G A G V V V P G V I R S G S V D A G A S I V V P
44104 GGCCGATCAGTTCGGTGGTGTGACCTTGCCCTCGACCAAGGCTCGACGCTGCCGAGGACGAACCGGTTTCATCTCCAGCATGTGCGCG
< G I L E T R D D V K G E V L P E V S G L V F R N M E L M D A
44916 AGGTTGCCGGTGCTCTCCAGTAGCCCGTGATGTTGGAGTCGACCCCGGTGGCCGGTTCGATCCACTGCACCGCGTCGGTGATCTC
< L N G T D K W Y G T I M T S D V R H G R D I M W Q V A D T I E
44288 CAGCTGTTGGCCAGGACGGCTTCAGCTCGGCCACGGCATCTGTGGACCAACCCGGGTGAAGACGTAGACCCCGACGAGGCCAGGTGCTCT
< L E N R W S P K L E A V A D H V V P S F V Y V G V L A L D S K
44380 TGGGGTGTCTCTCTCCACCCCGATCACCCGGCGCTCCGCGCCCATCTCGGCGACGCCGAAGGCGTCGGGTGCGGCGACCCGGGTC
< P H E P K E E V G I V R G D A G M E A V G F A H P D A V R T

FIG.11A(39)

44472 AGCATGATCTGCGGTGCGTCTCTGCGGAAGCGCTCGACGATGTCTTGATCCCGCCGACGATGAAGTTGTCCGCCGAGGTACATGAG
 <L M I Q A H P R E Q R F R E V I D K I G G V I F N D G L Y M V
 44564 GAAGTCGTGCTGCCGAGGTAGTCGCGGGAGATGAGCACGGCGTGCGCCAGCCCCGGGGAGCCTCTCTCGGGAAGGTAGGTACCTGGAGGCG
 <F D D D G L Y D R S I L V A H A L G R P A E Q P L Y T V Q L G
 44656 CGAACTGGGAACCATCGCCGACCACGGCTGAATTTCCGGGCGGGTGCTGCCGACGACGATGCCACCTCTCGATACCGCCCTCACCAGAATA
 <F Q S G D G V V R Q I E P A T S G V V I G V E E I G G E R I
 44748 GCCTCGAGCCCGTAGAACAGCACCGGCTTGTGGCCACGGGAATGAGTTGTTGGCGGACGTGTGGTGATCGGACGCAATCTCGATCCAC
 <A E L G Y F L V P K N A V P I L Q K A S T H T I P R L R S G V
 44840 CCCTCCCGCCAGGACCAGCGCCTTCACGAAACGCCCTCGAAAGGATGGGACCGAGACGGGTGCTGGTTACGAGCACTCCAGGGGTACCGG
 <G G A L V L A K V
 44931 TGGACTGGGCTCTTCGTGAACGTACCGAAGGATCACTCGTGAATTCCTACTTATGGGCCACCGAGGTGTGATCGGTGGATCTCTATGCGT
 < . A D
 45022 CCGCCATTTCCGCAACGGGGGCTGGCCGGCCGCGCCGACAGTTCGAGCACGGCGGCCAGGCCGTGCACGGTGTCCGGCGGGCTGGCC
 <A M E A F P P R A P G G G V L E L V A A L G H V T D P P S A
 45114 GGCAGCAGCAGGGTCTGCAGGCGGGTACACCGCCACCGTGGCCAGGGTGTGCCCCACCATCAGCGCCCGCTCCGGGGCGACCTTCAG
 <P L L L T Q L G A Y V A G G D A L T D G V M L A R E P A V K L
 45206 CTCGTGCAGGCGGTGCGGAAGATCCGGGGATCGGGCTTGACCGCCCCACCTCGTGGGAGAAGACGTAGGCGTCCACAGCTCCGCCATCC
 <E D C A T R F I R P D P K V A G V E H S F V Y A D V L E A M G
 45298 CGTACGCCGGAAGTGGGCCGAGGTCCAGGCGATGTTGCTGACCACGGCGGTGCCACGCCGCGCGGCGCAACTCCGCCAGGACCGGG
 <Y A A F T P R L D W A I N S V V A T G C G R R L E A L V P
 45390 GCGGCGTCGCGGTAGGCGAGCCGTCGTGCGGAACAGCCGGTCTGTAGAGCGCTCGGCGAGGCCGGGATGGGCGAGTTCGACGGTGGA
 <A A D R Y P L W G D T R F L R D Y L A E A L G P H P L D V T S
 45482 GAGCAGGCCACGTACGCGTGGGTGCGTTTCGGGCGGAGAGGTCCCGCGGGCGGTACACCTCGGCGAGCCCCGGCGGACGGCGTGGCGCT
 <L L G V Y A S R H T E P S L D R R A Y V E A L G P P V A H P E

FIG.11A(40)

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45574 CCGGCCCCGGGACGGCCGGCCAGCAGCAACCCGGTCAGGGCCTCCTGCTGCCCGGGTCGAGCTGGACGCCGACGGTGGCCGCCGCC
    < P G G P R G A A L L L G T L A E Q Q A P F L Q V G V T A A A
45666 GCCCGCAGCCAACGCTCGGCAGTTCACGGCGGAACAGCGTGCCGGAGAAGTCGAACAGGACGGCGTCGATCGGACGGGGCAGGGGGGTCGT
    < A R L W R Q P L E V A F L T G S F D F L V A D I P R P L P T T
45758 CATCGCTCTCCTCGGTGCAGCCGCTCAGGGCGGCACACGACCTGGCAGCGGACCAGCCGGATGTCCATCATGGAGGAATGCGCCGGGGTCG
    < M
45848 GCGCGCCCCGCCATGGCCGGTCCGGACGACAGGCATTTTGGTCACTCTTGCCTCTAGGCGGATTTCTTCAAAGATGGCTGTCAATTCT
45940 TTCAGCGATCCTGGAGGCATCCGTGACCCGTACCCGAACCGCCCTGGCGGGTGTCTGCCGCCGGTCTGGCCAGCCTCGCCACCCGCTGC
    > V T R T R T A L R R L L A A G L A S L A T A A
46030 CGCGACCTCTGTGCCACCGCCGGCCCGGGCGGCGGCCACCAACCCCGGCATCGACGTGTCCCACCTACCAGGGATCGATCAACTGGACGA
    > A T L V A T A G P A A A A T T P G I D V S H Y Q G S I N W T
46122 GCGTCCGCAACGCGGCATCCAGTTCGCGTTTCATCAAGGCCACCGAGGTACGAGTACAAGGACCCCAACTTCAACGCCAACTACGTCAAC
    > S V R N A G I Q F A F I K A T E G T S Y K D P N F N A N Y V N
46214 TCCTACAACGCCGGAGTGATCCGGGGGGGTACCACTTCGCGCGGCCGAACATCTCCTCCGGCGCCACCCAGGCCAACTACCTGGCCAGCAA
    > S Y N A G V I R G A Y H F A R P N I S S G A T Q A N Y L A S N
46306 CGCGCGCGCCTGGTCGGCGGACAGTCGACCCCTGCCGGCGCGGTGGACGTGAGGCCAACCCCGTACAGCGGCGCACGTGCTACGGCCTCA
    > G G A W S A D S R T L P A A L D V E A N P Y S G G T C Y G L
46398 GCACGTCCGGGATGCGTAGCTGGATCCAGGACTTCCTGAACACGTACAAGGCCCGCACCGCGCGGTACGCGGTCTATCTACACCACCGAGC
    > S T S G M R S W I Q D F L N T Y K A R T G R Y A V I Y T T T S
46490 TGGTGAACCAAGTCACCGGTAGCTGGACCGGGCGTGGGCCAACCCCGCTGTGGCTCGCCCGTGGTCGAGCACCCCGGCACCCCTGCC
    > W W N Q C T G S W T G P W A N H P L W L A R W S S T P G T L P
46582 GGCCGGCGCTTCGGTCTGGAGCTTCTGGCAGTACACGGCCTCCGGCAGCGTCTCCGGGATCAGCGGCAACGTGACCGCAACAACTGGGAACG
    > A G A S V W S F W Q Y T A S G S V S G I S G N V D R N N W N
46674 GCGACCGCACCCGGTGCAGCTGGCGAACAACACCTGACCCCGAACCGCCGGGTAGGCGGTGGCGGACGCGGAACCGGATTCGACCGGT
    > G D R T R L I A L A N N T .

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FIG.11A(41)

46765 ACGGTCGGCGCGGTCCGGCTGCCGCCAGCCCCGTACCCGGCCCCGGCTCGCGGGCCCGCCGGCATCCGGTCTCTCCGGCCCCGGGTGGCC
 46857 CGCCGTGCCATCCGCCAGGCGGCCACGCCTGGACGGGCGCGGCCACGACACCGAAGCGGAGACACCGGAGACCCGCGCTGACCCAG
 46949 CAGCAGCACACAGTCGCCGAAGGCGACGAGGATCCACAGTGCACGCCCGGGTCGAGCGTCCCTCGCTCGGTGCCATGTTCGACACCTCCCTCG
 47041 CATCGTCGGGATCAGATACCCCGTTCGACGCAAGTACATGCGAATCGACATCGCAACGGCGGGAATCGCCTGCTCAGCGGGCCGAGTCGGC
 47133 AATGACGGCCCCGGCGGCGCTCAGTCGACCCGGTCCGGCTTGAAGCCCTTGGCGATCCGGTCGAAGTCGGCCAGCCGCGCTGCCAGT
 < · D V R D P K F G K A I R D F D A L R A Q W D
 47224 CCTTGTCGCCACCTCCCACCGGAGGGCGTACCCCCGGTTGCTGGCCGTGACGAAGCCCCGGTTGCGGACGTGGATCCGAGTGCCGTCCCGG
 < K N A V E W R L A Y G R N S A T V F G R N R V H I R T G D R
 47316 TTCTCCAACCACTCCAGTCCGCGCACGTCTTGTAGTAGTCGCAGCGCTTGATGCTCAGATACTGGTAGCCGTTGACGTAGTTCTTCCGGGG
 < N E L W E W D A C T K Y Y D C R K I S L Y Q Y G N V Y N K R A
 47408 CGGTTCTTCTTTCAGTCGGCGTAGGCGTCGCCCTCCGGGGTGTGGTCCACTGCACCAGCAGCTCGCCACCCCGTCGGCTCGTCGA
 < P E K E K W D A Y A D G E P T S T W Q V L L E G V G D R E D F
 47500 AGACGATCGTGTCTGCCCCACGCTGGCGCGCACCCAGCCCTTCGGCAGGGGCGCGAGAAGCCCCGGGTCTTGTGCAGGAGCCAAACC
 < V I T N Q G V S R R V W G K P L P L S F G A P D K H L L W G
 47592 TCGGGCAGGGCGTTGCGGTCCACGGACGGGTGGCAGCGGCTCGGGCTGGCGGAGCCGCGCTGCTGGTCGCCGGTGCGGCGCACGGCGT
 < E P L A N P D V S P S A S P T P S P P A A S S T A P A A S P T
 47684 CGGCGTCGACACGCCCGCTGCGGGTCGCCCGGGCCCCGGGTGCTGTACCGCTCCGGCCGAGCAGCGCACCCGCCAGCAGGCGCGA
 < P T S V G A Q P D G G P G P D D D G S R G L L P V A A L L G I
 47776 TCAGCAGCACCGCAGCGCGCCGACAGAGCGCGGCGGCGACGCTCGGGCTTCGTGCCCCCGACGACGCTGGCCCGCGCTCGAC
 < L L V A V L A G V L L G R R R R E P K T G G V V T A R G T S
 47868 GAGAGTCCGGGCGGAGGCGCGCGCAGCAGCTCGGGGCGGCCCTCTCGGGGCGCGACGGCGGGCTCGCGGGCCGGGGCGGGCGG
 < S L A P G S A A P L V S T P A A E E R P A V A P E R A P A P P
 47960 CGAAACGGCACAGCCGCCCGGATCGACCCGGGTGTCGTGCGGTGTCGTGCGGCCGACCGCGCGCGCGCGCGCGCGCGCGCGCTT
 < S V P V A A G P D V R T D D A R T D D A R G A A P A G D A G E

FIG.11A(42)

48052 CGTCCCCAGCCTCGGGGGCCCGTCCGCCGGGGCCCGTCACTCCCTCCGGCCCGCGTGCCTCGTGGCGCTGGTCCGGCGTGG
 < D G A E A A R D A P P G D S G G A P T G A A E D A S T A A D
 48144 GGGGGGGGATCTTCGGGTGGGATCGGCCCGCTCGGGGGCGAAGTCGGTGACCTTCGGGTGGATCGGCTCGGCGCTCGGCAGGTCGAC
 < P A P I K A T P D A A Q P G F D T V K A T P D A D A S P L D V
 48236 CATCGCGTGGCGGGGTCCACCCCGCGGGACCTTCGGGTGGGTGCGCGCGCGCCACGCCGGCGCGCCGCCGCCACCGCGGCAA
 < M A T P A A D V G A P V K A T A D G G G V G A A A G G A A L
 48328 GACCACCTTCGGGGTACGGGTGCGGGCGGGCCGGTGGCTGTTGCGGGGGCGGTGCGGGCACCCACCGCGGTGCG
 < G G E P T R P A P P A A P R G T R Q E A P R P A P V V P P R
 48420 GGCTCGCGGGCGGTTCGGCCCCGGCGTACCGGTGAGCAGCGAGATGGTCTTGGCGGACGCCCGCGGGCGCGCGAGGAGCGG
 < P E R P G N P G P R R V G D L L S I T K A R R G A A R L L R
 48512 CTGGCCACCTCGGCTCGATCCGCTCGGCCGGTCTTCGGGAGCAGCCGTTCAAGCAGCGGTTCAAGGGCGGGCTTCCTCGGGCGG
 < E A V E A D I R E A P D K R L L G N L V P K L P G A N R P P
 48604 GCATCGGCTCGGTGGCCAGCGCCAGGTGGCGATCGCCAGCGTGGGGGAACGGCGACTTGCCCTCCACCGCGGTAGAGCGTCGG
 < M P E T A L A A L T A I A S P R A F P S K G E V A A Y L T A
 48696 CCCAGCAGCAGAGTCCGCCTCGGGCCGGGTGCGTCCGCGCCGCTCCGGGGCGATGTACGCCGGGAGCCACCATTCGCGT
 < G L S W L D A E P G A T G D R A R E P A I Y A P S G L V M G T
 48788 CCGGTCACGTTCCGGTACCGGGGATGGTCGACGGCCGAAATCGGTACGACCAACCCGCGCTCGGTGCCGAGCAGCACGTTGCCCGGCT
 < R T V N P D G P I T A L G F D T L V V R G D T G L L V N G P K
 48880 TGATGTCCCGTGCATGACGCCGGCCTTGTCGCGCCTTCAGCGCGCGAGCACCCCGCGATCTCGACCGCCTTGCGCGGGACACC
 < I D R H M V G A K H A A K L A G L V G L G I E V A K A P S V
 48972 GGCCCGTCTCCGGGAGAGTGCTGAAGGACTTCGACGCCACGTACTCCATGACGATCCACGGTGCCTCGGTCCGAGAACGTCGAA
 < P G D E A L T D Q L S K S A V Y E M V I W P D G D T R L V D F
 49064 GATCGGACCAGTTGACGTGGTTGATCGCGGATGGCAGGGCCCTCCGCGAGCGGCTTCCCGCATCTCGGGCGCTCCTCCGGGGTGA
 < I R V V N V H N L R A I A R A E R L S R E R M E R E P T L

FIG.11A(43)

49156 GGCTGGGCGGGACCAGTTCTTGATGCCACATCCCGGTGCAGCACCTCGTCGGCGGCTTCCATACCCGACCCCATGCCACCCCTGACC
 < S P P V L E K I A V D R H L V E D R A K W V R G M
 49247 GAGCGGCGAAATCAGCCGGTACCGGTGGGAACGAGTTGGGGAAGCGGTTTCGACATCGGTGGAGACGGTACCCGGGCGGCGGCCGCCGCAC
 49339 ACCGCGGCACGCCACTGTGCAGACGAAGTCAAGTTCCGACGCGTACGCTGAACGGCATGTCTGCCGAAGAGCCGCTGTTCCGGGTGACCC
 49431 GGGCGTTCCGACCGCGAGGAATGGCCCGGCTGGTCCGCGTTCATCGTCGCCCGGACCCGCTCCGCCCGGCTCAGCGCCCGCGCGCGG
 49523 TCGGCTGGGCACGACGGTGGCCCGGCTACGGTGTCTGCCGCTCGCCCGGAGCCTGGCGGCGCTCCGGTCTGCCCGCTGACGCGAC
 49615 TCGCCAGCATGTGGCCAGTGTGGCCCGCGCGGAGGCGGTGGCGGGGGCTCCCGGAGGTGACGACACCCGTTAACCTCACTCAGGGA
 49707 GACGATCCGTGACGGATAGGGAGGTCGATGATTCGCGAGGAGGACCGACACCTGGTTGAGCGGTACGGCAGCATCGAGGCGCGAC
 49799 ATCCGCCAGATGCGCGAGTTCCCGACAACTCCAGGCGGAGTTCGAGCGGAACACTACGCACCGCATCTGTCTACATAGCGGACGACATGAA
 49891 GGCACAGATCCCCAACCCCGCGACGCTTCGTGAACTGGTGCAGTTCTCAAGGCGCACACGAGACCCAGAGGCCACCGCCACGATGG
 49983 TCTGTCGTCGGTGGGGCCACCGCCACCTGGCCACGGCAGCGCGCGGATCGCCGAGCAGTACGCCGACTCCGACGCTTCTCCGCGCT
 50075 CGCGTCTCCGACGTGGAGCGGGCCCTCGCAACCGGGCGGGGCGAGGCGCGCCACGCGCGCTCGCCGACCCGACAGCCCGGA
 50167 CGGCGGCGCGGGCGGTGGTGTGTCATGATCGAGCGGGCAGCGGCGGAGCTCCGGCTCACCGACTGGCGGTGATGGACCTGCTGAG
 50259 CATGTGGCGTGCATCCAGGACACGAGACCGCGGCACTGGAAGCAGGTGCGCGGTGGCGCAAGTTTGGACCTCGCGCAGGCCACCC
 50351 TGGGCGCTCAAGGAGTACCGGCGGCTGGCGAGGCTGGCCACCGGCGACCAACGCGCGCGCCGCGGCGTACCTCGGCGAACTGGAC
 50443 GACCTGATCGACAAGGTGCAACGACCCACGACCGGCTGCCGCGAACTACGACGCTCGCGCGCGCCACCGAGCGATCAGCAGCGCCG
 50535 CACCGAACTCAAGCCGCTACACGACGAGTACGTGGAGAACTCCAGCAGAAGCGGGCGTACGAGGCGACTACCGCCGATCCGAAGGCGCTGA
 50627 TGGCAGCCGGCTGCCGGACAAGCCGGTGA CTGACGCGGACCTGGAACGACTCAACGCCAGGCCCGGAACCTGATGTACGGTTGAGCGGC
 50719 GAACTCCAACAGGCCCAAGCAATGCTCCGCCAACCCCTCTCCGCACCGCCCGGACGACAGCGGAACAACCCGGATGCTTACGAGAGCAC
 50811 AGGCACGCTCCGGTCA TCCGCGCTATTACAGTCCCAACCAATTAGGCTTCAATTCCTCAAGCGCTCAGCAAGCAGACGACGCCCTG
 50903 TTCCTGTCCAGAGCGCACCCCAACAGGTCTGTACTCGGGGGAATCGGGACGGGAACACCACTTCGCCCATCGGGCTCCATTTCTCCCGGC
 50995 ACCGGCCACCCAGTGACATCCAACCCGCGAGGAGTGTGGCCCTACCCTCCCGCGCAACTTGCCACCTGCCCATCGCCCCCTACGAGGAGG
 junction marker
 51087 CAGCACAACCGGCCAGGTAGGAACACGCCCCGTCAACCACGTCTCACGACCACTTCTTGCCAGGCGGCTGATCGGCGGGCGGCCCGGA
 51179 TGGGGATTAAACAACCCCTTGGCAATACTCTCCGCGAAGGATCAACCCAATTGGAGGGGTGATCGGGGGCGGTGGGGCTGGAACCTCACCA

FIG. 11A(44)

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51271 ACCGGCGCTGCAGGCACCTGCCCCGGGCTCGGGACGTGGTCCCCACCTTTAACCTGACCCCTGCGGGCCCTCCGAATGGCGCACCCGAAGGCGT
51363 CGTAAACACCTTAGGTCTGAATGGTGAGCCGTACGCTCATCCACCAGCGAGCAAGGCGATACTGACGGCCGCTACTGGGATCCCGACCATC
51455 CATGGGCAACCAAGCGAGGGCGTTCTCCAGTAGTCGGCCCGCCGAGGCGGAGGACCAATCGACCCAGGGCCAGCTATTGGCTTCGACCGG
51547 TGA AAAACGCTCCTCCAGCGGCGCTACCTTACCTTCCTAGCAACATTGATGGTTGCATCAGCGTACGCCCCGAGCGCCGTGCGTGCGGA
> V R A

51637 GTCCTGAAACCGATGGTGCCCTTGCGAATACGGGCTGACCAGTGGCACCTTAACTACCTGAAGGGCGGAGGCTCAGAAGCTGTCACTGGGA
>S P E T D G A L R I R A D Q W H L N Y L K A A E A Q K L S L G
51729 GAAGGGTTGTAGTAGCGGTCCCGGATACTGGCGTTGATCCACACCCCGACCTTCAGCGCAATCTAATCAAAGGGATTGACATCATTCGCCGG
>E G V V V A V P D T G V D P H P D L Q R N L I K G I D I I P G
51821 GGGCAATGGAGATGGCCAGAAAGATCGCAACAGTCAAGGCACTAGCATGGCTGGACTAATCGCAGCCCCACGGACAGGGCCAGAGCGGGCGCCT
> G N G D G Q K D R N S H G T S M A G L I A A H G Q Q S G A
51913 TAGGCATAGCACCCAGAGCAAGATCATGCCAATCCTGTCTTCGGCTGCAACAACCTCGGTGATGCAGACGGCTTGGCTGCGGGTATAGAA
>L G I A P R A K I M P I L S S A S N N L G D A D G L A A G I E
52005 TTTGCAATCTCGATGGGGCGGATGTCAATGTCTCCAGGGAGGGCGGCCAGGTTTCGACTCATCAAGGCAATCAGAGAGCGGTGCG
>F A I S H G A D V I N V S S G G A S V R L I K A I R E A V A
52097 CGCAGACATTGTAGTTGTCGAGCCGCGGAAACAGTCCGAAAGACATGACAATTGGCTATCCAGCCAGCGAGGAAGGAGTGTGCGCAGTTG
> A D I V V A A A G N S P E D M T I G Y P A S E E G V V A V
52189 GCGGAATTGATCGACAGGGAGAGCATGCTTCAGTTTCTGTCTGCGACCGGAAGTTGACTTAGTCGACCGCGCAGTCGACATCTACAGCACC
>G G I D R Q G E H A S V S V V G P E V D L V A P A V D I Y S T
52281 AGTTACGACGGGAAGTACTCCAAGGCACCGGTACGTCCAGTGCACAGCGATAGTCGAGGGCCGCTGCTCTGGTCCGATCGAAGTTTCC
>S Y D G K Y S K G T G T S S A T A I V A G A A L V R S K F P
52373 CGACCTGCCCGCCTCGGAGGTGTCCTCATCGCCTCACTGCCACCGCCCATCGACAAGGGCCGCCAGGGCACGACGACGACGACGACGACGACG
> D L P A S E V V H R L T A T A I D K G P P G H D D Q Y G Y G
52465 TTATCGACCTGGTTGCCGCGCTTACGGCAGACGTACCCCCGGTGGGCTTTGAGTCGGCGACGGCGGACGTGCCCCGACGTGCGCTGGGTGACCC
>V I D L V A A L T A D V P P V G F E S A T A D V P D V P G S T

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FIG.11A(45)

52557 ACGACGGCGGTGCGCCGAGCCGGCAGGCGAGGTGACGATGGGGCAACGGCCCCGAGGTCCTGGCCACGTTGGGAGTGATCGTGGCTGCTGCGGG
> T T A V A E P A G E G D D G A T A R G L A T L G V I V A A G
52649 CGCTTGGGCGCTGGTGCCTCGACGGCGTAGGTTGAGCGACGACCCGCCCGGGATCAGCCGGTGACCGCCAGCCCTGACGCCATGTGCG
> A W A L V A R R R L S D D P P P R I S R .
52740 GCGACATTGGGGGTGGGTGGGATACCGCTATTGGCCGACATGAAGTCGATCAACAGCGATCAACAGGCAGTGTGATCGGCGGGG
52832 GTCGGTCGACGGCCAGGCGGCGTCGACGGAGGGGGGAAGCGGTAGCGTCGGCGACGTGCCGAACTCGATTTCACCTCCGACTCGTGCCTCGC
> V P N S I S L R L V L A
52924 GTCGGCGAGCCCTGCCCCGTGCGAAGCTCCTCCACGGCCGCGGCATCGAACCCGACGTGCTGGTCAGTGGGTGCGACGAGTCCCAGGTGACCA
> S A S P A R R K L L H A A A G I E P D V L V S G V D E S Q V T
53016 GCGAGCGAGCCGAGGATCTGTGCCTGGAGCTGGCCCGCCTGAAGGCGCAGGCGGTGCTCGGCCGGCTGCGCCCGTGGCCGACGAGCGGACG
> S E R A E D L C L E L A R L K A Q A V V G R L R P S A D E R T
53108 CTGGTCTCGGCTCGACTCGGTGCTGCGCTTCGACCGGAGATTCTCGGCAAGCCGCGCAGGCGGACGCTACCCGGCGTTGGGAGCG
> L V L G C D S V L A F D R E I L G K P A D E A D A T R R W E R
53200 GATCGGGGGCGCAGCGGGGTGCTACACACCGGGCACTGCCTGATCGACGTATCCACGAGACGCGCGCGAGGCGGTGCGCTCGACCAACG
> M R G R S G V L H T G H C L I D V I H E T R A E A V A S T T
53292 TGCCTTCGCTGACATCAGCGACGAGGAGATTGCCGGTACGTGCGACGGCGCAACCGCTCGCGGTGCGCGCGCGTTACCATCGACGGA
> V R F A D I S D E E I A A Y V A T G E P L A V A G A F T I D G
53384 ATGGCGGGGCGTTCTGGAGGGTGTGACGGGACCCGGGCACGGTGGTGGCCCTCTCCCTACCGTTGCTGCGCCGGCTTCTCGGCGAGCT
> M G G A F L E G V D G D P G T V V G L S L P L L R L L G E L
53476 GGACCTGCGGATCATCGACCTGTGGACGAAGTGTGCGCGGGCGGCCAGGCGGTGAGGCGGTGGGTACGGTCCAGCCATGACGACGAAGT
> M T T K
> D L R I I D L W T K V A P G G Q A V E A V G T V Q P .
53567 CCCTGCCGCTGACCCCGAACTGCATGCGTACGTGGTGGCCCGGATCGGACCCGCGGAGGTGATCGGGGATCTGATCGAGGAGACCCCTC
> S L P L T P E L H A Y V V A H G S D P D E V M R D L I E E T L

FIG. 11A(46)

53659 GCCCGCGTCCCCGAGCGAGGATGCAGGTGGCCCCGGAGCAAGCCGCGTTCCCTGACGTTCCCTACCCGGTTGATCGGGGCGCGCGGGC
> A A L P A E A R M Q V A P E Q A A F L T F L T R L I G A R R A
53751 GGTGGAGGTGGCACCTTCACCGGCGCTGTCTCCTGGCGATCGCGCGGGGCTGGCCGAGGGCGGGCGGTGACCTGCTTCGACATCTCGG
> V E V G T F T G L S S L A I A R G L A E G G R L T C F D I S
53843 AGGAGTACACGGGCGTCCGCGCGGTACTGGGCGCGGGTGGCCGAGACAGATCGACCTGCGGATCGGGCGGGCGGGGACACGCTG
> E E Y T G V A R R Y W A R A G V A D Q I D L R Y G P A G D T L
53935 CGCGGGTTGCCGTACGAACGGCACCTGGACTTCGCGTTTCATCGACGGGACAAGGTGGGTACCCGGTCTACTGGCGGGAGTTGGTGCCTCG
> R G L P Y E R H L D F A F I D A D K V G Y P V Y W A E L V P R
54027 CATGCTCCCGGGGGTTCATCGCGGTGGACAACACGTTGCGGGGGCGGGTGTCTGCCCCGCGTGACGCCGACGCCGGCCATCGCCG
> M L P G G V I A V D N T L R G G R V L A P R D A D R A I A
54119 CGTTCAACGACGAGGTGATGGCCGACGTCCGGGTGGAGCCGGTGTCTGCCGATCGCCGACGGGTGACCTGGCCCCGGGTGCGCTGACG
> A F N D E V M A D V R V E P V L L P I A D G L T L A R V R .
54210 GCGCCAGCGGACGATCGTCCAGGTGCGCGGCGCGGTGTGTGTCCGCTCACCGGTTCACGAGGGGTGACGAGGGGTGAGCGGGCGGGGTGT
54302 AGGAAGGGGCCCTTCTATACCGAATGCGTTAACAAAGGGGCCCTCCTTACACCTCAACCTACGCGCACGCTGCGGGCGAACTGGCGGGCG
< . R V S R A F Q R A
54393 GCCCAGGCGACGCGGCGGCAAGCACCGCGATGATGGTCAGGCCCTGCCAGACCTTGCTGTTGCCGAGGTGCGCGCGCAAGAGGGCCCG
< A W A V G V A A L V A I I T L G Q W V K D N G L D G A F L A R
54485 GGTGCGTCCACGGCCAGGAGAACGGGTTCACCTCGGCGATGCGCTGGAGCCAGCCGGGGCGAAGGTGAGCGGCAGCAGGATGCCGGAGA
< T G D V A W S F P N W E A I R Q L W G P A F T L P L L I G S L
54577 GCAGCAGCACCGGTGGCGGACGGTGTTCATACCGGGGGAGCGGCTCCTACCTCTTGACCTTGAGCGCGACGCCGTACGAGACGGCCGAG
< L L V P Q A V T N M V P A L A D E S K V K L A V G Y S V A S
54669 GTCATCAGCGCGATCAGGGCGAGCATCAGGTACGCCAGCAGCAGGTCCCGATGAACACGCGCAGCTCGAACAGGAGCGCGAGCGGTGAT
< T M L A I L A L M L Y A L L L D G I F V R L E F L L A L L T I
54761 GATGACGGCCTGGGCGAGCAGCAGCTCGCGCAGGGCCCCGGCCGAGCAGCGCGGCTGACCCGGGTGACCCGGGGACCCGGGACCGTT
< I V A Q A L L S V V D R L A R G L L L A L R S V P T V R S R E

FIG.11A(47)

54853 CGATACGCCGGCGCAGCTCGGCGATCAGGCCGAAGCCCTGGAAGAGGCCGCCGAAGATGGCCAGCAGCACCAGCAGGCCGGGCACGAAG
< I V G A R L E A I L G F G Q F L G G F I A L L V L L G P V F
54945 ATCTTGACGCCTCGGCCTGGGTGCGCGCTTACGCCGGGCTTGAGCAGCGGGGCGAAGAGGAGCAGGTACATCACC GGCTGGAAGACGCC
< I K Y A E A Q T P A N L A P K L L P A F L L L Y N V P Q F V G
55037 GACGAAGACCCAGACCGGATTGCGGAGCAGGAGTTGCATCTGGCGTGGGCGACGAGCCAGGTGTGCGGGCGGAACCTTCATGATCGGACT
< V F V W V P N R L L L Q M Q R Q A V L W T D R A F K M
55127 CCGGGTGT CAGGACTCGCGCAGCGAGCGCGGCTTGGTGAGGAAGACGTCTGAGGCTGGGGCGGTGCAGCTCGATCGAGCTGAGCC
< • S E R L S R G T K T L F V D D L S P R H L E I S S L R
55218 TGAGGCCGACTGGTCGAGCCGGCGCAGGACCTGCGGGATGGCGTGGCCCCCTCGTCGACGGTCAGGGCGCAGGCCGCCGCTCGACGGTT
< L G S Q D L R R L V Q P I A T A G E D V T L R L G G D V T
55310 TCCAGCTTGGTACGTACGGTCTGGTGTGAGCAGTTGGGCGCGCGGGTGGCGGCTCCAGCCGACGAGCAGCACCTCGCCCGGA
< E L K T V Y P E T D L L Q A A Q P T A A D L G V L L V E G S
55402 GATCTCCGCTTCAGCCCGCCGGGTACCTCGGCGACCACTCGCGTGGTCCATGATCGGATCCGGTCGAGAGCGGTCGGCCTCGT
< I E R K L G G P T G E A V V E G H D M I A I R D C L A D A E D
55494 CCAGGTAGTGGTGATGAAGACGGTCACTCCCTCGGCGCGCAGCGGATCTGTCACACATGTGGCGCGACTCTGCGGGTCGAGG
< L Y H T T I F V T M G E A R L R R I E D W M H A R S Q P D L
55586 CCGTGGTGGCTCGTCCAGGAAGACAATCGGGGGTGTGGATGATGCCGAGAGCGATCTCGACGCGGCGCGCTGGCCGCGGAGTAGGT
< G S T P E D L F V I R P D H I I G L A I E V R R R Q G G S Y T
55678 CTTGCACTTACGGTCGGGCTACTCGGTGAGCTGGAAGCGCGCCAGTCGCGCTCGGCGGGGAGGGCGTGGCCCTTGGCGATGCCGTACA
< K C K R D A Y E T L Q F A A L A R E A R R L A D A K G I G Y M
55770 TCCGGGCGTGCAGGACCACTTCTCGGCGCGGTGGAGTCGTCCGGTGTCCGCGCTGGGCGACATAGCCGATCCGGCGACGACCTCG
< R A H L V L E E R A T S D D W T S G G Q A V Y G I R R R V E
55862 GCCGGGTTCCGCAGCAGGTGCGGCCCGCGGATGGTGGCCTGGCCCGCTCGGGGGTGTAGGGGTGGCCAGCATCCGCAGGGTGGTGTCTT
< A P N R L L D A G A I T A Q G G D P T I L T A L M R L T T K

FIG.11A(48)

55954 CCGGGCGCGTTGGGGCCGAGGAACCCGAAGATCTCCCTCGGGGACGTCCAGGTGCGACGGCGGACGGCGTCGACCGTCTTGTGCTGTC
< G A G N P G L F G F I E G E A V D L D V G R V A D V T K H Q R
56046 GACCGGGCGGGAGCGAAACGACTTCGCGAGCCCTCTGGTCTGGATCATCTTCGCTCCTGTCGTCTTAGCCGGACCGGGCCGGCCCTC
< G A R S R F S K R L G R T Q I M
56136 TCTCCGGGACGCCACGCCACACGGGTGGCCCGAAGCTGCGCGGAGGCTAACCGGATATAACTCTCTAGTCAACTTTGATTATATGGCGA
< • R S I V E R T L K S • H R
56227 CCGTCGGCCCCCTCCCCACGTTCCAGCCGTCCTGACTGGCCAACCCCTTCGGGCAGATACGGCACGCCGGCCTCGATCCGGTCGGGACCCG
< G D A G E G V N W G D Q S A L G E P L Y P V G A E I R D A V R
56319 CTCACACGAGCCACCTCGACCTCTCCCCGGGAATCCACAGCTCGTACATCCAGTCAAGCCGACCGGCTTGGAGTCGGGATCCAGGAGG
< E C W A V E V E G R A I W L E Y M W S V G V P K S D R I W S S
56411 ACTCCATCGAGGCACGCATGGTTTCGACACTGGCCCCGCGCACCTGCCCCGACTGGCGAGCGGGGCCACCGCCTCCGGCCTGGGCAGCGCC
< E M S A R M T E V S A R L V Q G R S R L A A V A E P R P L A
56503 GGCAGGAACGCCGCGCCACGAACGGATCGTCTGATGATTGCCCCACCACAGGCCGCGCAGCAGCGTCTCGAACTCGTCGACCCCC
< P L F A F A A V F P D S T Q H N G W L G R L L T E F E D V G
56595 CTTCCGGGTGATCTCGTACGTCTGTCGCGCGCGCGGCGCGACCTGCTCGTGGCGACCTCGCGGAGCAGCCCTCCTCGCCGAGCTTGC
< K P T I E Y T T R A R R A G V Q E T A V E R L L G E E G L K R
56687 GCAGCGGTGTAGATCGAGCGGGCTGCACGTTGGCCCACTTGTGGCACCCCAACTGAGCAGCTCGCGGGGAGCGTCTGTAGCCGTGCACC
< L A H Y I S G P Q V N A W K D A G W S L L E R R V D Y G H V
56779 GGCTGCATCCACTTGACCAGGCGCGAGAATCATATCGAGTGGCAGACACCGGAAAAGATATTAGACAAGTTTGACTATCCAAGCATCTG
< P Q M W K V L G L I M M
56870 GGCAGTGCCTCATCCACACTGAGCGATCGTTAGGGCCACGACGCCGGCCGATAAACTCCCGTCAGTAACATCCCGGGAGGACCCAGAG
56961 GTGCGCAAGGTACTCATGCCAACCGAGGCGAGATCGCCGTCCGCGTATCCGGCGCTGCCGCGACGCCGGCCTGGGCAGCGTCGCCGTCT
> V R K V L I A N R G E I A V R V I R A C R D A G L G S V A V
57052 ACGCGGACTCCGACCGGGACGCCCTGCACGCGACCCTGGCCGACGAGGCGTACGCCCTGGGGGGGACACCGCCCGGAGACGTACCTGCGG
> Y A D S D R D A L H A T L A D E A Y A L G G D T A A E T Y L R

FIG.11A(49)

57144 ATCGACAAGCTGATCGCCGTGCGGGCACAGCCGGGGCCGACCCCGGTACGGCTTCTCGCCGAGAACGCCGACTTCGCCCA
> I D K L I A V A A Q A G A D A V H P C Y G F L A E N A D F A Q
57236 GGCGTCTCGACGCCGGGCTTACCTGGATCGGCCCGACCCACAGCGGATCCGGGACCTGGGGCACAAGGTCACCGCCCGGCACATCGCCC
> A V L D A G L T W I G P T P Q A I R D L G D K V T A R H I A
57328 AGCGGGCCGGCCCTGGTTCCCGGTACCTCGGACCGGTGCGCAGCCGGACGAGGTGATCGCATTCGCGGTGACCAACGGCCTGCCG
> Q R A G A P L V P G T S D P V G S P D E V I A F A V D H G L P
57420 GTCGCCATCAAGCCGCCTTCGGCGGGCGGGCGGGCCTCAAGGTGGCCCGCACGATGGAGGAGATCCCGCACCTGTTGAGTCGGCCAC
> V A I K A A F G G G R G L K V A R T M E E I P H L F E S A T
57512 CCGGAGGCGGTGCGCGGGGTTCGGCCGGGGCGAGTGTTCGTGAGCGGTACCTCGACAGCCCGGCACGTCGAGGCCAGGTCTCTGCGCG
> R E A V A A F G R G E C F V E R Y L D Q P R H V E A Q V L A
57604 ACCAGCACGGCAACGTGATCGTCGGCACCCGGGACTGCTCGTAACGCGGACCCAGAAACTCGTCGAGGAGGCCCCCGCGGTTTC
> D Q H G N V I V V G T R D C S L Q R R H Q K L V E E A P A P F
57696 CTCACCGACGCCCGGCAGATCCACGACAGCGCCAAGCAATCTGCCGGGAGGCCGGTACCACGGCGCCGCACCGTGGAGTACCT
> L T D A Q R R Q I H D S A K A I C R E A G Y H G A G T V E Y L
57788 GGTGGGCACGGACGGACGATCTCTTCTTGAGGTCAACACCCGCTGCAGGTGAGCACCCCGGTACCCGAGGAACCCGCGCATCGACC
> V G T D G T I S F L E V N T R L Q V E H P V T E E T A G I D
57880 TCGTCCGCGAGCAGTTCGGGATCGCCGACGGCGAGAAGTGCGGCTGGCCGAGGATCCGACCCCGCGGGGCACTCCATCGAGTTCGGGATC
> L V R E Q F R I A D G E K L R L A E D P T P R G H S I E F R I
57972 AACGGCGAGGATCCGGGCGCAACTTCTGCCCCCGGACCGTCACCGCGCTGCGGCTGCCACCGGCCCGGTGCCGGTGGACAC
> N G E D P G R N F L P A P G T V T A L R L P T G P G V R V D T
58064 CGGCATCTCCGCGGACGTGATCGGCGCAACTTCGACTCCCTGCTGGCCAAGTGATCATCAGGGCGAGACCCGCACCGAGGCCCTGG
> G I S A G D V I G G N F D S L L A K V I I T G E T R T E A L
58156 AGCGGGCCGGCGGTGGACGAGATGGTCGAGGAATGGCCACGGCGTCCGCTCCACCGCTGGTGTACGGACCCCGCGGTTTC
> E R A R R A L D E M V V E G M A T A L P F H R L V V R D P A F

FIG.11A(50)

58248 ACCGCCGCCGTTACCGTGCACACCCGGTGGATCGAGACGGAGTTCGACAAACACCGTCTGCCGTTACCGCCGCCGCCGCCGCCGCGA
> T A A P F T V H T R W I E T E F D N T V L P F T A A A G P A E
58340 GGGCCCGCCGAGCGGGAGACCGTGTGTCGAGGTGGCGGCAAGCGGCTGGAGGTGACCCCTCCCGCCGGCCTCGGCGCGGGTACGGCCG
> G P A E R E T V V V E V G G K R L E V T L P A G L G A G T A
58432 CCGGGCCCGCCGCGGAAGCCGCCCGGGGGCGGGGGCAAGCCGGCGGGGTGGCGGCGACGCCCTCACCTCTCCGATGCAG
> A G P A A R K P A R R G G A K A G A A V G G D A L T S P M Q
58524 GGCACGATCGTGAAGATCGCCGTCGCGGACGGGGACACCGTCGCCAAGGGCGACCTGTGCTGCTGGAGGCGATGAAGATGGAGCAGCC
> G T I V K I A V A D G D T V A K G D L V V V L E A M K M E Q P
58616 GCTGCACGCGACAAGCGGGCACGGTCGGCGGGCTGTCCGCCGAGGTGCGCGCGGTCTCGCGCGCGGCCCCCATCTGCACCATCACCT
> L H A H K A G T V G G L S A E V G A V L A A G A P I C T I T
58708 GAGGTGCAAGGAGGGCCCCCTGTTAACGCATTGGTATAGGAAGGGCCCCCTTCCTAACCCACGCGCCCGGGCGCGCCAGCCCGGG
> •
58800 TACGCGTACCGGCCGCCGGGTGTTTTCCGCGACCACCGGAGCGGTGAGGACCGGGGCGGGGAATGATGGCCAGGTGCGGTTCTACATGGC
> > V R F L H G
58891 GCGGTTCCCGCCACGACCTGACCTACAACGACGTCTTCATGGCGCCGAACCGCTCCGAGGTGCGGTCCCGTTGGACGTCGACCTGGCCAC
> A V P A H D L T Y N D V F M A P N R S E V G S R L D V C L A T
58983 CTCCGACGGCACGGGCACCACCATCCCGCTGGTGGTGGCAACATGACGGCGGTGGCGCGCGCGGATGGCCGAGACTGTGCCCCGGCGGG
> S D G T G T T I P L V V A N M T A V A G R R M A E T V A R R
59075 GCGCACTCGCGGTGATCCCGCAGGACATCCCGATCGAGGTGGTGGCCAAACGTGGTCGCCCTGGGTCAAGCAACGGCACCTGGTGCACGACAG
> G A L A V I P Q D I P I E V V A N V V A W V K Q R H L V H D T
59167 GCGATCAGCTCGGCCCCACCGACACCGTCGGCGATGCCATCTGCTGCCGAAACGGTCGTCATGGCGCGGTGGTGGTGGTGCAGGAGGC
> A I T L G P T D T V G D A I H L L P K R S H G A V V V V D E A
59259 CGGTCCGCCGCTGGGCGTGGTGACGGAGGGACACCGTCGGGGTGGACCGCTTCGCCCCAGCTCCGCCACGTGATGTCGACCGAGTTGCACA
> G R P L G V V T E A D T V G V D R F A W L R H V M S T E L H

FIG.11A(51)

59351 CGGTCCGGCGGACGGACCGGTACGGATTGACCGGCTCTCGGCGGGCGGGCGGGCTCGGCCGGTGGTGGACGGCGACGGCCGG
>T V P A D A D P R T G F D R L S A G R R R L A P V V D G D G R
59443 CTGTCGGGGTGTGACCCGCAAGGGCGCGTGC GCGGACCTCTACACCCGGGGTGGACGACCGGGGCCGGCTGCGGATCGCGGGCGGC
>L V G V L T R K G A L R A T L Y T P A V D D R G R L R I A A A
59535 CGTCGGCATCAACGGCGACGTACCGGCAAGGCCGCGCGTGTGAGCGGGGTGACGCCCTGGTGGTGACACCGCGCACGGCCACC
>V G I N G D V T G K A A A L L E A G V D A L V V D T A H G H
59627 AGGCGCGGATGGTCGCCCGCGTGC GGGCGGTGCGCAAGCTTACCCGGGGTTCCGGTCGGCGCGGCAACGTGGTCAACCGCGGATGGGGTA
>Q A R M V A A L R A V R K L H P G V P V A A G N V V T A D G V
59719 CGCGACCTCGTAGGCCGCGCGACATCGTGAAGTGGCGTCGGTCGGGCGCATGTGCACCAACCGGATGATACCGGGGTGGGGCG
>R D L V E A G A D I V K V G V G P G A M C T T R M M T G V G R
59811 TCCGCAGTTCTCCGGGTGCTGGACTGCGCGGCGCGCGGACCTCGGGCGCACGTCTGGCGCGACGGCGGGTACGGCACCCGCGCG
>P Q F S A V L D C A A A R D L G R H V W A D G G V R H P R
59903 ACGTGGCGCTGGCCCTCGCCGCGCGCGTGAACGTGATCGGTTCTGTTGCGCGGCACGTACGAGTCCCCGGTGACCTGTACACG
>D V A L A L A A G A S N V M I G S W F A G T Y E S P G D L Y T
59995 GACGCGACGGCCGGAGGTACAAGGAGAGCTTCGGGATGGCTCGTCGGGGGGTCAAGCGCGGTACGGCCGAGGACAGCGCTTCGACCG
>D A D G R R Y K E S F G M A S S R A V S A R T A E D S A F D R
60087 GGCCCGCAAGGGGATCTTCGAGGAGGGCATCTCTCGGCCCGGATGATCTGACCCCGGATCGACCCGGGCTCGAGGACCTGATCGACGAGA
>A R K G I F E E G I S S A R M Y L D P D R P G V E D L I D E
60179 TCATCTCGGGGTACGCAGCGGTGCACGTACGCGGGCGCGGAGCTGGCGGAGTTCGGGAGCGGGCGCTGGTGGGGTGCAGAGCACG
>I I S G V R S A C T Y A G A R S L A E F A E R A L V G V Q S T
60271 GCCGGTACACGAGGGGATGCCCTACCGACGAGTTGGTGACCCCGCGCGCGGTGAGAAGGTTCCCTCTCTACCGGAGGCGGTCAA
>A G Y T E G M P L P T S W .
60362 CAAGGGGCCCTTCCTTCGTGCGGCTGGGTATCGGCGTGACCGACTGCCGCGACGGCGCGCCGACACTGAGCCGCCCGCGCTCGAGGGCCCC

FIG.11A(52)

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60454 ACCGAACGGGCGCGGGTCACTGAAGAGCGGACGGATGACGGTCCGGGCGGGCCCTCCGGGTCCGGGCCGGTGCCGGGCGGAGCGCC
      < • D F L R R I V T R A A A E P D P G T G P P L A
60455 CCGGCCAGCCAGAGTGTACGAAGCCGTGCACGATGACACAGGCGGCCAGGGCGTCGGCCTCCTGGTCCGGGTCCGTTTCCCGGCGGGGAG
      < G A L W L T V F G H V I S W A A L A D A E Q D P D T E R R P L
60637 GGCGGCCACCCCGGCCGAGCGCGCGGCCGATCACGGCGGCTGTACCTCGGGGTCTGCGACGCTAGAGCTCCGGGCGGAACA
      < A A V G A R L A A G A R D R A A T V E P D D R R Y L E P R F M
60729 TCACCTGAAGTGGGCCCGGTGGTCGACCGCGAACCAGGTACGCCACGCCGGCGTCGAGCAGGTGCGCGGCCCTCGCACAGCGCCCGGCC
      < V E F H A R H D V A F R V Y A V G A D L L L D G A E C L A G A
60821 AGCAGGTCGAATCCCTCGACGGCGAGCGGTTAGCAGCCCCGCTTGTGCCGAAGTGGTGCGCGGGGGCGGCGTGCGAGACCCCGGCCCG
      < L L D F G E V A L A T L L G A K D G F H A P A A H S V G A R
60913 GCGGGCCAGGTCGCGCAGGCTCAGGGCGGCCCGCGCTGGTGATCGGTGACGGCGGCGGAGCAGGGCGGACGCGAGGTCACCGT
      < R A L D R L S L A A P G A D T I A D V A A A L L A R R L D G H
61005 GATGGTAGCCACGGTCCGGTCATGCCGCGAGCCTAACTTGTCATTGACAAGATAGCCAGGCGCGAAGCAATCTAGGCAATGACAAGTTG
      < H Y G R P G T M
61095 CCTTCGACCGAGGAGAACCCCGATGGCGCCCTGATCGCTCTCATCGCCGGCTCGGCCCTGGCCCCGACTCGCCGGGCTACTCAACGTCGACG
61187 CCCTGGCCGGCTGGCACCCCGCCCTGCGGGTCGGGCTCGCGGCATGTTGCGGCTACCGGGATCGCCCCACTTCACCTCCCGACGGCCCCGAC
61279 CTGGTCGCCATGGTGCCGCCCGGACTGCCCCACCGGGGCTGCTGGTGACCGTACCGGCCCTGCTGGAGTTGGCCGGCGGTCGCGCTGCT
      > M V P P R L P H P G L L V T V T G L L E L A G A V A L L
61371 CGTCCCCGGCACGGCGGTTGGGACGGCGGGGCTGGGGCTGCTGCTGCGGATGTTCCCGGCCAACGCCCTCGGCCGCCGCGCGGGC
      > V P G T A R W A A A G L G L L L A M F P A N A S A A R R G
61463 TGACCTGGCCGGCGCGGTGACCCCGCTGTCCTCCCGCGGCTGCTCCAGGTGATCTTCTCACCGCCGCGCGGATTCGTTTGGG
      > L T L A G R P V T P L V P R A L L Q V I F L T A A A I S F G
61555 CCCTGACTATCAGGGAGCTAACATGACCCGCGATGGAGCTGATAGGGCTGCGAGACGTGCCACTCGGCCGGCTGCTGGTACC CGCGGCCA
      > P •

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FIG.11A(53)

61645 CGTCGTCGGCCAACGGTGGAAACCGCTACCTGCGCGAGGACACGGCCTCACCCAGGCGGGCATGGTCAACCTGATGACCCCTGGCCCGGCACG
 > V V G Q R W N R Y L A E E H G L T Q A G M V T L M T L A R H
 61737 GCGAGCTGCCGACCGGGCGGTGCGCGAGGCGTGTTCATCGCCCGGCCACCTAACCGGCATCGTCGACACACTGGAGCGCGACGGCCTC
 >G E L P H R A V A E A C F I R P A T L T G I V D T L E R D G L
 61829 GTCGAGCGCAACGCGACGCTGACCGGGCGAGGTGCGGCTCGTCTGACCCCGCGCGGTGGGAACGGGTGCGCGCGTCAACCAACGT
 >V E R Q R D D V D R R S V R L V L T P A G R E R V A A L T N V
 61921 CATGCAGTCGGACGACCGATGACCTCGGTGACGCCGACCCGGGAAGCGCGGTGATCCGGCAGTTCCTGCTCGAGGTCAATCGGCAGTG
 > M Q S G R P M T S V D A D P A K A A V I R Q F L L E V I G S
 62013 GAGAGGAACCTCGGGTGACGGCCCTCGACGCGAGCGCGAGGCTCCGGCATGCTGATCCGGTGTCTCGCGGCCACCTGGCGCCGTACCGTC
 >G E E P R V T A L D A R P E A P A C .
 62105 GACCGCTGGCGGGGTGATGGCGTTGCAGTTCGTGGCACGATGGCCTCGCTACCTGCCGAGCCTCAACGCCGACATCATCGACCAAGG
 > M A L Q F V G T M A S L Y L P S L N A D I I D Q G
 62196 TGTGGCCCGGGCGACACCGGTACATCATGCTACGGCGGCTGGATGCTGTGTGAGCCTGGTGCAGATCGCCTGCTCCACCGCCGCGG
 > V A R G D T G Y I M R T G G W M L L V S L V Q I A C S T A A
 62288 TCTTCCTCGGCGCGCTCCGCGATGGGCTTCGGCCGGGACGTACGCGCGAGGTCTTCGCCCCACGTCAACCGTTCTCCGCCCGGAGGTG
 >V F L G A R S A M G F G R D V R A E V F A H V N R F S A R E V
 62380 ACCCGCTTCGGCGCACCCCTCGCTGATCACCCGCAACACCAACGACGTGCAACAGGTGCAGATGCTCGTCTGATGAGTGCACCATGCTGGT
 >T R F G A P S L I T R N T N D V Q Q V Q M L V L M S C T M L V
 62472 CGCCGCGCGATCATGAGCGTCGGCGGGGTGTTTCATGGCACTGCGGGAGGACGTGCGGCTGTCCTGGCTGATGCTGGTCAAGCGTGCCGCGC
 > A A P I M S V G G V F M A L R E D V G L S W L M L V S V P A
 62564 TGGCGATCGCCCTGATGTCGTCGCGGATGTCGCCGGGTTCGGGTGATGCAGACCCGCGCATCGACGGGTCAACCGGTGCTGCGC
 >L A I A L M L I I R R M V P G F R L M Q T R I D A V N R V L R
 62656 GAGCAGATCACCGGCATCCGGGTGTCGGGCGTTCGTCCGCGAGCCGTACGAGACGGCGGCTTCGGCCGCGGGAACGCCGACCTCACCGC
 > E Q I T G I R V V R A F V R E P Y E T A R F G R A N A D L T A

FIG.11A(54)

62748 GACCGCCCTGCGCACCGGTCGGTTGATGGCCCTGATCTTCCCGTGGTGACGCTGGTGCTCAACGCTCTCCAGCGTGCCGCTGCTGTGGTTCCG
> T A L R T G R L M A L I F P V V T L V L N V S S V A V L W F
62840 GCGCGGACCGGCTGACGCGCGCCAGATCCAGGTCGGCGGCTCACCGCCCTTCTGCAGTACCTCATGCAGATCCTGATGGCCGTCATGTTG
>G A D R V D A G Q I Q V G A L T A F L Q Y L M Q I L M A V M L
62932 GCCACCTTCATCCTGATGTTCCCGCGCGCGGTTCTGCGCGAGCGGATGTCGAGGTGCTCGACACCGACTCGACGGTGATCCCGCC
> A T F I L M M V P R A A V C A E R I V E V L D T D S T V I P P
63024 GCGCGCGCGACGGCCGAGGTGACCGGCCGGGGCGAACTGGAACTGCGCGGCTCCGGTTCCAGTACCCGGGGCGAGCGCGGCTGCTGC
> A A P T A E V T G R G E L E L R G V R F Q Y P G A S A P V L
63116 ACGACATCTGTTCCGGGCCACGCCCGGGCGCACCGCCATCATCGGACGACGGGGCGCGCAAGACGACCCCTGCTGACGCTGATCCCC
>H D I S F R A T P G R T T A I I G S T G A G K T T L L T L I P
63208 CGGCTGATCGACGCCACCGCGGGCGGTGCTGGTCGACGGGTGGACGTGGTGACCTGGCCCCCGGACGATTTGTGGCGCGGATCGGGCT
> R L I D A T A G A V L V D G V D V R D L A P D D L W R I G L
63300 GGTGCCGACGGCGGTACCTGTTACGGGCACGATGCCAGCAACCTGCGGTACGGCAACCCGGACCCACCGCGGAGCTGTGGGCCG
> V P Q R P Y L F S G T I A S N L R Y G N P D A T D A E L W A
63392 CCCTGGAGATGCCCCAGGCGCGGACTTCGTGCGCGAGTTGCCGAAGGCTGAACGCCCCCGATCACGCAGGGGCGCACCAATATCTCCGGC
>A L E I A Q A R D F V A E L P E G L N A P I T Q G G T N I S G
63484 GGGCAGCGCCAGCGCTCGCGATCGCCCGGGCCCTGGTCCGAAGCCGGAGATCTACCTGTTTCGACGACTCGTTCTCGGCGCTCGACCTGGG
> G Q R Q R L A I A R A L V R K P E I Y L F D D S F S A L D L G
63576 CACCGACGCCCGGCTGCGCGCGGCGCTACGACCGGTACCGCGGACGCGACGGTGCTGATCGTGGCCCCAGCGGGTCTCCACGATCGTCGACG
> T D A R L R A A L R P V T A D A T V L I V A Q R V S T I V D
63668 CCGACCAGATCATGTGCTTGAGGACGGGGCATCGTCGGGATGGGCCGACACGCCGAACACTACTGGAAGACTGCCCGACGTACGCGGAGATC
>A D Q I I V L E D G G I V G M G R H A E L L E D C P T Y A E I
63760 GTCGCCTCCAGCAGCGCGGGGTGCCGGCATGACGGCCGTACCGGATCAGCGGCCCCACCGCGCGCGGGCGGGGCGGAGGGCCGACGCCGAA
> V A S Q Q T A G V P A .

FIG.11A(55)

63851 GCGGCTGCCCTCCGGCAACAGGGCAGCGGCCCGAGGTGGATGAGCGCCGGCATGCCGGCCGAGAAAGTCGATGAAC TTCGGGCCGTCCAC
> M S A G M P A E K S M N F G P S T
63941 CCGCGGGTGTGCGCCGGGTGCGACCGCACCGCTCCAGCTGGCCGCCATCGTCTGCTCGTGGTCAGCGTCGGTTGCAACGTGTACG
> R R L L R R L R P H R L Q L A A I V L L S L V S V G C N V Y
64033 GGCCGAAGGTGCTCGGCCACGCCACCGACCTGATCTTCAGCGGGTGATCGGCCGGCAGTTGCCGGCCGGCACCAACCGCCGAGCAGCGGTC
> G P K V L G H A T D L I F S G V I G R Q L P A G T T A E Q A V
64125 GCGGGGCCCGCGCGCGGTAAACGACAGCTTCGCCGACATGTGCCCGGATGGACGTGGTGC CGGGTGGCATCGACTTCACCGCCCT
> A A R A A G N D S F A D M L A R M D V V P G V G I D F T A L
64217 GGGCGGGTGTGCTGTCTGCTCGCCCTCTACCTGGCGGCCAGCGTGTGTTGTGGTGGCAGGGTGGCTGCTCAACGGGGTGGTGCAGC
> G R V L L F V L A L Y L A A S V L L W W Q G W L L N G V V Q
64309 GCACGGTGTGCGGGTCCGCGCGACGTGGAGGACAAGCTGAACCGGTGCCGTGCCGTACTTCGACCGGCAGCCCCGGGCGAGTTGCTC
> R T V L R L R A D V E D K L N R L O L O Y F D R Q P R G E L L
64401 AGCCGGTACCACGACATCGACAACATCTCGCAGAGCCTCCAGCAGACGCTGAGCCAGCTGCTACCTCGCTCACCGTGGTCGGCGT
> S R V T N D I D N I S Q S L Q Q T L S Q L L T S L L T V V G V
64493 ACTGGCCATGATGTTCTGGATCTCGCCGCTGTGGCGTGGTCCCTGGTCGCGGTGCCGATGTCGGTGGTGGTACCAGCCTGGTCGCGA
> L A M M F W I S P L L A L V S L V A V P M S V V V T S L V A
64585 AGCGGTCACAGCAGCGTTTCATCGCCAGTGGACGCATACCGGAGAGCTGAACGGCCAGATCGAGGAGCGTTACCGGACACGAGCTGGTC
> K R S Q Q R F I A Q W T H T G E L N G Q I E E A F T G H E L V
64677 AAGGTTTCGGCCGGCAGCGGAGGTGGAGCGCCTTCACCGCCAAGAACGAGGAGCTGTTCGGGGCCAGTTTCGGGGCCAGTTTCATCTC
> K V F G R Q R E V E A A F T A K N E E L F R A S F G A Q F I S
64769 CGGGATCATATCGCGCGGATGATGTTTCATCGGGAACCTCAGTACGTCCGATCGCCGTGGTTCGGCGGGCTCGGGGTGGCGTCGGGGTCGA
> G I I M P A M M F I G N L S Y V A I A V V G G L R V A S G S
64861 TGAGCATCGGCGACGTGCAGGCATTTCACGACTCCCTCCAGTTACCCAGCGCTGACCCGGGTCCGCTCGATGGCCAACCTGCTCCAG
> M S I G D V Q A F I Q Y S L Q F T Q P L T R V A S M A N L L Q

FIG.11A(56)

64953 TCCGGGTGGCCTCCGCCGAGCGGGTGTTCGGGTGCTCGACGCCGAGGAGCAGAGCCGGACCCGGCGGTGCCGGCCGGGTGCGCGACCA
> S G V A S A E R V F A V L D A E E Q S P D P A V P A R V A D Q
65045 GCGCGGTGCGTCGAATTCGACCACGTCTATTCCGGTACGAGCCGGACAAGCCGCTGATCACCGACCTGTCGCTGGTCGCCGAGCCGGGGC
> R G R V E F D H V S F R Y E P D K P L I T D L S L V A E P G
65137 ACACGGTTGCCATCGTCGGGCCGACCCGGCCGGAAGACCAACCTGGTCAACCTGGTGATGCGCTTCTACGAGCTGGACGCCGGCCGGATC
> H T V A I V G P T G A G K T T L V N L V M R F Y E L D A G R I
65229 ACCCTCGACGGGTGACATCACACGCTGAGCCGCGACGACCTGCGCGCGGATCGGCATGGTGCTCCAGGACACCTGGCTCTTCGGTGG
> T L D G V D I T T L S R D D L R G R I G M V L Q D T E L F G G
65321 CACGATCCGCGACAACATCGCGTACGGCCGGCCGACGCGAGGAGGAGATCGTCGCCGCCCGCGGCGACGTTCTGTGGACCGGTTCTG
> T I R D N I A Y G R P D A S E E I V A A A R A T F V D R F
65413 TGCGTAGCCTCCCGACGGCTACGACACCGTCATCGACTCCGAGGGCAGCAACGTAGCGCCGGCAGAGCAGCTCATCACCATCGCCCGG
> V R S L P D G T D T V I D S E G S N V S A G E K Q L I T I A R
65505 GCGTTCCTGGCCGAGCCGTGCTGATCCTCGACGAGGCGACCAAGTTCCGTGGACACCCGACGGAGGTGCTGTCCAACGGGCCATGGC
> A F L A E P S L L I L D E A T S S V D T R T E V L L Q R A M A
65597 GCGCTGCGCTCGGACCGGACCAAGCTTCGTATCGCCCAACCGTTTGCCACCATCCGCGACGCGGACCTGATCTGATGAGCAGGTC
> A L R S D R T S F V I A H R L S T I R D A D L I L M E H G
65689 GCATGTCGAGCGGACCCACGAGCAGCTCCTGGCCGCCCGGGCGGTACCAACCGGCTTACCAGGCCAGTTCACCCAGCCGGACCCG
> R I V E Q G T H E Q L L A A R G A Y H R L Y A Q A F T Q P D P
65781 GCCGCCGTGGGGACCCGAGCCCCAGCCCGCTCGGTCCGGGGCTGACCGTCTGTGGCCCGGTACATCCCGCCAGCTCCCCGACCCGAG
> A A V G D P E P Q P A S V R G .
65872 GGGAGCTCCCGGGCCCCGGCGCGGAAGACAGAGCGTGGTCCGGGAGAGCGCCGGGAGACGAACCTGCTGTCGGGGCCAGCCG
65964 CATCGCGGGAACATGTCGTCGGCGAAGTGGCCGAGGTGCGGGCCCTCGATGACGGTGACGTACGTGCGGGCGCGGGGTTCCTCCGACGTCG
66056 TGGTCCGTACCGCGCTGGCGATGGGAGACGGTAGCCCGCCCGGGGGCGGCGCATCCGAATTCGGGGCCGGCCGACGACGCCGAGACG
66148 CATCCGTTACCGCGAAGGGGACAGGCCGCCAGTCGCTACAGTCGGCAACCCGGCCGATGCACAGCGCGCTCGGGGCGGGCCGCCGAC

FIG.11A(57)

66240 GGGACCTGCCGGGGCCCATGGCGGCCCGGTGTCGGGTACGGGGGGTCCGACACTCGAGGCGCGCCGACTACGGTACGCCGGCCGTCGGC
66332 GATCCGCGACCGCCTCCACCCGTACGCCGAGGTTCGGGGCCCAAGGGTCCCGGCCCGCGCGGTGCCCGAGCCGCGCTGCCGGGCC
66424 GACGACCCGGTTCGTGGCGGTGCCCGCGAGGTGGAGCCGCCAGTTACTCCAGCTCGTGGAGCATGAGCTGGCGGGCGCCTCGGTGATC
< . E L E H L M L Q R A A E T I
66515 GAGCCCGACAGGCTCGGGTAGATGGTGATGGTCTGGGCCAACTCGTTGACCGTGAGGTTGTTCTCCACCGCCATGGTGATCGGCAGGATCAG
<S G S L S P Y I T I T Q A L E N V T L N N E V A M T I P L I L
66607 CTCGCTGGCCTTCGGTGCCACCAACACCGCCGATCACCTGGCCGCTGGCCGGCGGCAGAACAGCTTCACGAAGCCGTCGGCGAGGTCGT
<E S A K P A V V G G I V Q G S A P R C G L K V F G D A L D D
66699 CCATCTTCGCCCGGGGCTTGGCCGACAGCGGACGATCACCTGGCGGGCCGGGTCTTGCCGGCGTCCACCTCGTCTGGGAGACGCCGACG
< M K A R A N G S L P L M V Q R A P T K G A S V E D Q S V G V
66791 GTGGCCAACCTCCGGTCGGTGAAGACGTTTCGGGCCACCGTACGACGCCAGCGGCGGACCGCCCTCGCCGAGCGCGTCCACATCGCGAT
<T A L E P D T F V N A A V T R L R L P R V A E G L A H W M A I
66883 CCGGCCCTGCATGGCGGCGACGCTGGCCAGCGGCAACACCCCGTGCAGTCGCGCGGACGCTAGATCCCGGGGACGTTGGTCGGGACACCC
<R G Q M A A V S A L P L V G T C D G A A Y I G P V N T R S V R
66975 GGTGACGGTGACGTAGCCGCCCCGGGCCAGCTCGACGCCGTACTCGGCGAGGCCGAGGTTGGCGGTGGGGATCGAGCCGACCGCGATG
< D V T V Y G G R A L E V G T E A L G L N A T N P I S G V A I
67067 AGCGCGTGCAGCCGTGCACCGCGCCGTCGGCCAGTTCGACCTCCACCCCGTCGGCGATGCGCTGGACCTCTCGGCGGGGAGTTGTT
<L A H S G H V L R G D A L E V E V G D A I R Q V R E A R S N N
67159 GAGGATCGTCATGCCCCGGGAGCGGAACACGCGCTCGATCGCCATGGCGGCGTCGGCGTCCCTCGTGGGCATCACCCGTCGCGGTGGAGA
< L I T M G R S R F V R E I A M A A D A D E H P M V R D R S S V
67251 CGAGGTGACCGGGACCCCATGGCCAGGTACGCGTGGCGAACTCGGCACCGGTGACGCCGGAACCGACGACGATCAGGTGCTCGGGCAGG
< L T V P V G M A L Y A S A F E A G T V G S G V V I L H E P L
67343 TGGCGCAGGTCTACACCTGCCGCCAGGTACGATGCGCTCGCCGTCCGGCACGGCCGTGGGAGCTGGCGGGGGTGGCGCCGCGGTGGCGAC
<H P L D Y V Q E W T L I R E G D P V A T P L Q R P T A G T A V

FIG.11A(58)

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67435 CAGCACGGTCGACGGCTGATCGAGTGCTTCTCGGAGCCGTCGGCCGGCGTGACGACGCGGGTGGGTGGCCAGCATGTCTCGCCGA
    < L V T S A D I S H K E S G D A P T V V R H T H G L M D E G L
67527 GCCGGCCGTGCCGGCCACGAAGGTGACCGCGCTTTCACAGCTTCGCGTGATGTCGGCGGACTGGGCCAGGGCAGCGCTTGACCCGC
    < R A T G A V F T V G A K V L K A H I D A S Q A L A L R K V R
67619 TCGTGACGGCCGGCGTCGACGGTGACCGCTCCAGCCCGTCGGAGTGACCCCGAACTCCTCGGTGTCCCGGTACCCGGTGACCACTC
    < E H V A R A D V T V A E L G D S H V G F E E T D R Y G T V V E
67711 CGAGCTGGCGATGAACGTTTTTCGACGGTAGCGAGTCGGACAGCACGAGCACCGCGGCCCTCGGCCTCCACCACGGTGACATCAGCGT
    < S S A I F T K S P V C D S L V C A G G A G E A E V T V D A D
67803 CCAACTGGCGCGCAGGGCCGCTCGTACCGGCGGCCCGCCCGGATGATCAGCATCTGGCTCACAGCTATCGCCCTCGTCCGT
    < L Q A A V L A A E Y G A P G G I I V I Q S V
67893 GCTCACAGTGACTTCTCTCCCGACGCTCCGACACGACCGTCGTATTCTCCCCAGCCGTCGCGCGGGCTATCGTCATCGCCGTGCG
    > V R

67984 TCACTACGCCGCCTACGGCTCAAACCTGGACCCCGCCGGATCGCGGCTACTGCCCGCACTCCCCGATGGTCGGCTGGCTGGAGG
    > H Y A A Y G S N L D P A R M R A U C P H S P M V G V G W L E
68076 GCTGGCGGCTACCTTCGCGGGTGAGGGCGCGATCGGCTGGGAGGGCGCGGTGAGCACCATCTGTCGAGTCCCCCGGTGATCGGGTGTCTGTG
    > G W R L T F A G E G A I G W E G A V S T I V E S P G D R V F V
68168 GCGCTCTACGACATCCACCGTACGACGCCGTCCAGCTCGACGAGATCGAGGGGTGGCCTCCGGGACGTACCGCAAGCTGCACGTCCGCGT
    > A L Y D I H P Y D A V Q L D E I E G V A S G T Y R K L H V R V
68260 CTCCACCTCGACGGCGACGTGACCGGTGGGTCTACGTCTTCGACGGGTACGAGGGGGCGCTGCCGACGGCGTGGTATCTGTCGGAGATCG
    > S T L D G D V T A W V Y V F D G Y E G G L P T A W Y L S E I
68352 CCAACGCCCGGAGAAGGGGGCGGCCGACGACTAGTCAAGGAGCTGCGGTCCCGCCCGCCACCGGACGGGTCGGCGTAGCGCGTCTC
    > A N A A E K A G A P D D Y V S E L R S R P T G T A S A .

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FIG.11A(59)

68443 CCACACTCCAGTCTGCTCCGCCCGAGACGGGGCCGCACGGCGGCCCCCGGGGGTCTGTCTGTACACATCATGGTCGCGCCCGTACACA
< . V
68534 CCGCCGTGGCGGGGACGGTGCCTCGTACATGTCGGTCCAGCGCATCTCGCGCAGCCCCACCGAGCGGTAGAGCGTCGCCGGGGAGGTC
< A T A A P V T R E Y M D T W R M E R L G V S R Y L T A P S T
68626 GGGTTGGTCAGGTCGACGCCGAGGCCGGCTGCCGCCGTCCCTTCGCCGCGTAGACCGTGAAGGCCCGCCACAGCAGCGCGCGCCGACCC
<P N T L D V G L G A H R R G K A A Y V T F A R W L L A A G V G
68718 GTGCCGCCGTACTTCGGCAGCACCGACAGGGTCCGCACCCAGCCGAGTCTGTTCAGCGCCTGGTCGGACGACTGCAACGCGCCGGCCG
<H R R Y K P L V S L T R V W G S D Q W L A Q D S S Q L A G A P
68810 GCTCCCCGTGACCTCGGCGACGAACCACTCGTCCAGGTCTGTCTGACGGGGCAGACGCTCCCGCCAGTGGTCGTACCCGGCCGGCTCG
< E G D V E A V F W E D W T R D Y A P L R E R W H D Y G A P E
68902 TAGTCCGGGGTGTCCCGGAACGCCGTGTCTGATCCGGTGAACAGCGCAGGTCTCTCTGTCGCCGGCGCGCAGCGCGCCGACCGTCAC
<Y D P T D R F A T D Y I R H F L R L D D E D G A R L P R V T V
68994 CCCGGGTGGGGCGGGCTCGGCGGCGAGCCCCGGCCAGGTCACGACTCATCCGTACGTACCCGGTTCACCCGGCTGAAACCGGCCTCGGTCA
<G P P P P E A P L G A L D R S M R V Y R K V R S F G A E T L
69086 GCTCCGTACCCAGCGGGTCTCCGGCGGGTAGGCCGAGGCCGACGGTCAAGCGGGCAGGCTCCGCTCCGGGGCCCGCTCGGCGACCCCGG
< E T V W R T E P P Y A S A R V T L A P L S R E A A R E A V R
69178 TCCAGCATCAGAGCGAGCGGGGCGGTACCGCTCGGCCGCTCCGGGTCCGACGAGGACGTCGACGAAC TCCGGGCCACCCCGGTCCG
<D L M L A L L P A R V A E A R E P D V L V D V F E R G V G T P
69270 GTTGTCCACCACGAGCGAGCCGGCCCTGCGGGTCTGACCAAGCAGGAGTCCGGCGCGGGTCAAGAGGGGGCGGTCAAGGGGGCGTCAAGG
<N D V V D Q A V L R G Q P D S V L W S D R A P D F F P A T L A
69362 CGGCCTTGACGTCTTCGGCGTCGAAGTCCGGGTGCCCGATCGCGAAGGTGTCTCGGGCGTGCACGACGCGGAGGATCCAGGGACGTCGTCTG
< A K V D E A D F D P H G I A F T D A A H V V A L I G P V D D
69454 AGGTGGGGCGCGCCCGCCAGTCAGCGGAAGAGTCAGGGGGGATCTGGCAGCACCCCGGTCCCGGCCCTCATTTTCAACCGC
<L T P R R A A W D A P L T V

FIG.11A(60)

69545 CCGGGCCCTGCCCGCCGCGCACGCGCTCGCCGGCGAGAGGGGACCCTTTCTACCCAGGGGTTAGTAAGGGGCCCTTCTTGCAACCAC
< . Y P A R G Q V V
69637 GGGGGTGGGTGAGCAGGTCGAGCAGCGCGGTGCCCTCGGCCGGGTGAGCGCCGGGAATCCGGTCGACACCAAGCGGTGCGTCAACCG
< A R A T T L L D L L A T G E A P T L A R F G T S V L R D R V A
69729 CCTCCGACCACAGCGGGCGGCACCAAGCGGCCGACCCGGGGGTACGGCGGGCAGCGCGCAGGCCAGCGCCCCGGCCTCCCCCTCCGGC
< E S W L R R V L P G V R P Y P P W G C A L A G A E G E P
69821 CCGGCCAGCACCGCCTCCAGCGGCGTCATCCCGCGGCCCGCACCGCAGGTCAGCCCCGGCGAAGTGCTCCCGAAGCAGCAGCAGCCCC
< G A L V A E L P T M G G A R V A L L Y A G A F H E R L L L L G
69913 GGGGGGGCACGGGGCCCCGGGTGTCTCGGGCGGCGCACGGCCCCAGCGCGCAAGAGTGGCATCCCGTGGCGTCCGGCGGCTCGA
< A A R A G P T D D P P V A R W A A F L P , G S A D A A D V
70005 CCACCCGGTGCAGCGGTGCCAGAGGATCACGGCGGCACGGCGGTGAGGTGCTGCTGCCCCACCGGCAGCACTCGGCCAGGTTCGCC
< V R H L L T A L R I V G P V A T L H E S G W R C C E A L N A
70097 GTGGCCACCTCCAGCGGAGGTGCACGGGGGGGGGTCCACCCGTGGCGACCGGTGGGGGGCGACGAAGCCGAGGGCCGCTCAC
< T A V E L P A H V R A A A D W G S A V A D P A V F G L A A S V
70189 CGTGGGGCCCCGACGTGCGCGAGCACCCCGGGCCGGCGGATGTGGAAGGCCAGCCGGAGATGCCCAGCAGACGGGCCCGGTGCAGGG
< T A A G V D G L V G A R G A I H F A Q G S I G L L R A R H L T
70281 TGGCCGGCAGCGGGCGAACATCTCCCGAGCTCCAGCACCAACGGCTTGCTCGCGGGCGGACCTGCTCCGGCGTCATCGGGTTCAGTCT
< A P C R A F M E G L E L V L P K S A A A V Q E P T M < . D
70372 GCCCGCGGGGCTTCGGTGACAGCCCCGTCTTCGGCGTCGACCGCCTCGATCGCCCCCTCGATTTCGCCGGTGGCGGCGGTGGGGGGGT
< A G G P G E T V A G D E A D V A E I A G E I E G T R R Q A A T
70464 GACGGCCGTTCCGGCCGCGCGGGCCAGCTTCGGCCGGCTGAGTTCTGCTGGCCCTCGCGCGGATCGCTCCAGCTCGGCCAGCGACC
< V A R E A A R R A L K R R S L E Q E A E A R S R E L E A L S R

FIG.11A(61)

70556 GCTCGATGCCGGTCAGTTCCTCGGCACCGTGTGCTCGGCCCTCCACGGCGCGGCCAGCTCCGCCCTCGGCCCGCTCCTGGTGGTACGGCC
< E I G T L E E A G D H E A E V A G A L E A E A R E Q D T R A
70648 CGCGCCAGTTCCTCCAGCATCCGGCGTTGCCGGGCCCGCTCGGCACGGGCGCGCGCTCGGCCCTCCGGGGCGCCGCTTCGCGCGCGG
< R A L E R E L M R R Q R A R E A R A A R E A E R A A R K A R P
70740 TGGTGGGTGGGCGGTGGCTGCTCCTCGCCGCCGTGACCAACGGAGCTGGGGGCGGGCACCTCGCCGAAGCCGGCGTAGCTGGCGG
< P P H T P P Q E E G G T V L R L Q P R P V E G F G A Y S A A
70832 CCCGCAGCAGCCGGCCGGAGCGCACCTGCCCGGCCACCTCCGTGTGCGAGAGCGCGGCTCGAGCGTCGCCCTCCACCTCGCCACGCGGCAGC
< R L L R G S R V Q G A V E T D S L A A D L T A E V E G L P L
70924 TTCCCGCGCGCGGCCCGCCCTCGGCGTGGCGGCCAGCCGGCGCCTCGGCGACCAAGCGGCGACCGCCGCCCGCTGGGCGGAGAG
< K G A P P G G E A D A A L R R A E A V L A A V A A R R Q A S L
71016 TTCCCGCAGCCGGGGCCGCGCAGGTGCGCTGGGCGCGCGCAGCGCTCGGCGAGTTGGGTAGGTGCGCGACCACTCGGGGCGGCGCA
< E R L R P G R L D R Q A R R L A E A L Q T L D A V L E P R R L
71108 GGGCGAGCAGGTTGACCAGCCACGGGCCACGGTCGGCGCGCGCAGCCGGCGGATCTCGCGGCGCTGCGCGGCGCTGCGGAGCGCGGGCC
< A L L N V L W A A V T P R R L R A I E R A T A P D G S R R A
71200 TCGGCGACGGCGGCTCGCGGTGGCGACGAAC TTCTCCGGCGCTCGGTGTAGAGCCGCGGAGGAGGCTCTCGGGGGCGGCACGGCTC
< E A V A A D R T A V F K E P P E T Y L R R L L S Q P P V < .
71291 AGACGTCGAGCCGGCTGCCCGGCTCGAGGCGCTGGTAGTCCCGACAGCGCGGCTACTGACGGTTGAGGACGGCGAGCCGTTGTGCG
< V D L R S G P O E L R Q U D T G S L A A Y Q R N L V A L G N D
71383 TTGAGCAGCCCGTGTGAGGGGAAGGCTCGGCGCGGGGCGACCGCGGGATGAAGTCGAGCACCTCGGAGAACTTCGACCAGGGGCGGTG
< N L L G D H L A F A R R P A V A R I F D L V E S F K S W P A H
71475 GATCGGCGGAAGAGGTGTCCACGGGGCGTCTCGGGTGCCACCAAGGGCGTCCCGGGGTGGTAGACGACGCTGTTTCAGCAGATACCCGA
< I P A F L T D V P A D E P A V L A D G P H Y V V D N L L Y G L

FIG.11A(62)

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71567 GGTGTCCACGACGGGATGTGGGATGGATGACGGCGTGCAGCCGCGTACGGCGGCACCGCCACGCCCGCGCGGTGAACGCCTGCCCG
      < N D V V P I D P H I V A H R G G Y A R V A V G A A T F A Q G
71659 GGTGAGATGGGCTCCAGGGCTTCGGCCACGTGCGCGAGGGCACCGGCCAGCGAGGCCGGCGGTAGATCGGGAACGGCCAGCGGTGAGCTG
      < P S I P E L A E A V D G L A G A L S A P G Y I R F P W R D L Q
71751 CCGGGTGAGAGCCGCGACGTCCACGTGGTGGGGTGCTCATGGGTGATCAGCACCGCGTCCGACCGGTCCAGCGCGGTGCGGTGCTGAAGA
      < R T L A A V D V H D P H E H T I L V A D A G D L A T P D S F V
71843 CGCCCGGTGACGACCAAGCACACCGCGTGTGCTCGACGCGGAGGAGTGCGGCAATTTGGTGAGCTGCATCGTGACTCCTCGAT
      < G P D V V L V G G D H E V R L C S H A F K T L Q M
71933 TGACCCAATCGTGATGCCCTCAGCGCAGTCTGCCGGAACCGCGCGGTGCCGCTCGCTGAGGTATCGCCCGATGGGGCGTAGACGAT
72025 CGGAGCGGGAATGGACGGACACGCAAGACGAGGTGCTGACCGCGGTGGGGCTGGTGGCGTCTGCTGGCGCGCGGTGGTTGCAGCGCCGACA
72117 GCGATGGGGCGGAGAGCCTTCGGCGCGGTGGCGCCCGAGCAGCGGCGCACCTGCCGACGGGGCAAGCGGAGCAGGGTGCCGATGCCGGG
72209 GGAACGCGGTCCGGCGCGGTGGCGGCTCACCGGACCTGCGGGTCGACCAAGCGGTCAATCATCTACACCGGAACCATGCGGGTGCGGGTGG
      > M R V R V
72300 ACGATGTGGACGCCGCCCGGTCCGCCATCACGGCGGTACCGGGTGGCGGGCTTCGTGGCGCGGCACGAGCGCAGCGCGGAACC
      > D D V D A A A R S A I T A V T G V G G F V G G D E R S S G G T
72392 GCCGACGCCCGGGGAGTTGCAACTGCGGGTGCCGGCGGAGCGGTTACGGGCCGTCTGGAGGAGTTGGCGAGGCTCGGCCGCGAGGACA
      > A D A R A E L Q L R V P A E R F T A V L E E L A R L G R Q E Q
72484 GCGGGCGATCCGCACGGAGGACGTGACCGAGGAGACCGTGGATCTCGACGCGCGGATCGCCACCCACGGGCCCGGGTCGAGAGCGGTGCA
      > R A I R T E D V T E E T V D L D A R I A T Q R A R V E S G R
72576 AGTGTGGCGGGCCACCTCGATCGGCGACCTGGTGACGCTGGAGAGCGAGGTGGCTAGGCGGGAGGCCGACCTCGCCTCGCTGGAGGCG
      > K L L A R A T S I G D L V T L E S E V A R R E A D L A S L E A
72668 AAGAAGCGCGGTGGCCGACCTGACCTCGCTCTCCACCATCACCCCTGCTGGTCCGGAGCGGAGGCCCGGACACCGAGCCCCGA
      > K K R R L A D L T S L S T I T L T L V G P E A E A R D T E P D
72760 CACCGGCTTCGTGGTGGCCTGCGCGCGGCTGGACGGCGTTGTCGCCCTCGCTGGCGGTGCTGCTACCGTGTCTGGGGCGCTGCTGCCGT
      > T G F V V G L R G G W T A F V A S L G V L L T V L G A L L P

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FIG.11A(63)

72852 TCGCGGTGGCCCTCGGCGTGCCGGTGGCGGTGCTGCTTGCGGTGCTGCGGCGGCGCGGCGTGCACCGCCGGCGCGCGGTCAACGCGCC
>F A V A L G V P V A V L L A V L R R R R P P A P A V N A P
< . R A
72943 GCCGCCAGTCCCCGAGCGGGTCTGCACCATGACCCGGATGCCGACCGGATGGCCCCCTCGTCGACGTGCAACGAGGCCCGGTGCAGGT
> P P V P A A R S A P .
<A A L A R L A T Q V M V R I G V A I A G E D V D F S A R H L D
73034 CGACGTTGGGCGGACCGGCGGACGCGGAGGGGGCCAGCGCGCGGGGACGTACTCCAGGTACCAAGAGAAGTCTCGCCGCCCATGCTC
< V N P G S R G V G L R A L A G P V Y E L Y W S F D E G M S
73126 TCGGGGTCTCGGCGACCCCTCCGGGCGAGCGGCGTGGGTGCGCGCGGTGAGCACCTGGATCGCCCGGGCGTGTGGTCACCGGCGG
<Q P T E A V G E P G L A A H T A A T L V Q I A R A D N T V P P
73218 CCGGCCGCGTAGGTACTCCAGGTCGACGGTGGCGCGCGGTGGGGCGATGACGTCCGCGACCACTGAGCGACGATCTTGGGGCCTGGTCCC
<R G R L Y E L D V T A G T P A I V D R V V Q A V I K P A Q D W
73310 AGGTGTCGGGTCCATACCCGCGAGGTGCCGGACGCGGACGCTCGGACGGGATCACGTTGTACCGGTGCCGGCGGAGCGGTGGCCGAAC
< T D R D M V R L T G S A S A E S P I V N Y R T G A S A H G F
73402 ACGAGCAGACCCGCTGTTGGCCGGCACCCGGCGGTGACCAGGGCTGGCACCTCGGTGACCAGCCGGCGGCGGCGTCCGACGAGTCGAC
<V L L L G S N A P V R R S V L A P V E T V L R G L A D V L D V
73494 GGTACGGTGGGGGAGCGGTGTGCCCGCGGGGCGGTGAGCCGGACGGTGACGTTGTGCGGCGGCGGCGGTGATCGGGCCGACCCGCGAGGC
<T L H P R A T H G G P G T L R V T V N D A A A T I P G V E L G
73586 CGACCTTGCCGACGGGTGTTGGGTGCGAGTGCAGTCCGAAGATCTGCACGACGTCGTCGAGACCGCGGCGCTCGATGACCTCCAGCGAG
< V K G V P Q N P D V H L A F I Q V V D D L G G A E I V E L S
73678 CCGCAGGGCAGGATCTCTCGGCGGGTGGAAAGATCAGCCGGACCCGGCGCTCCAATTCGCCGAGGTTGGCGAGTTGGGCCAGCAGCAGCC
<G C P L I E E A P Q F I L R V R G D L E G L N A L Q A L L V G
73770 GACGCCGAGCAGCGGTGTGCACGTGTTGGCCGCGAGCGGTGGCAGACACCGTCTTGGTGGACCGGTAGGGCACGTCTTGACGTCGG
< V G L L V T T H V D H G C A H C V G D K T S R Y P V D K V D T

FIG.11A(64)

73862 TCAGGGCAGCGGTCGATGTGGGCGGAGCGGACACCGGGCGTCGGGGCGCGTCGATGTGCAGATGACCCGTTGCCCTTTGGC
< L P L A D I D A R L A V V P G D P R G D I D C I V G N G K P
73954 AGCAGGCGGGCGCAACCGGCGAGCAGCTCGGGGCGATCAGGGCCGCGTCTCGAACTCCTGCGCGGAGAGCTCCGGTGGGAGTG
< L L R P R L G A L S L E R A I L A A T E F E G S L E P H S H
74046 GATGTGCCGGGTGGCGATAAGGCCGGGCATCCGGAGGGCGAGCAGATGGTCGAGCTCGAAGGGCAAAAGGCTGCGACCCGACGGCGGACT
< I H R R T A I L G P M R L A L L H D L E F P L P Q S G S P S E
74138 CCGGCCAGGCCGACGCCAGGTGGCTGCCGTTCCGCAGCGTCAACGCACTCGTCAGTCGAAATCTCGATCACTAGAAACGGATGGATC
< P W A S S A L H S G N P L T L A S T V
74229 ATCAGGGATGACAGCGCCAGCCTAGACCTTCGACGGTGACTCTGTGCAACATCATTCCCGTAGCGATCGGACCGCGCAGCGTCACGAATAC
74321 CCTGGTGAAGGCTCCATAATCTCGGGACAGCAGGTAGATCGCGTTGAACGGCGTCATCTGCCCCCCACCTCCTACAACCCGTAACCGA
74413 TTCGGCGGTACGAAATCACCGTCGATCCGGGGCGCTGCTACCGAATTGTGCAATTAGTCGTCICGGTTAACTGCCGCTCGGACAAGTAAC
74505 CGACCGCACTCGGCAGTCGGACGACTCCGACGGTGACACGAGGGCCGACCTGCTCCCGCACATGCTGTCCGTCCCAATCACCCGGACGGG
74597 TTACCCACTGCCCCGGTGGCACACCGGGCTGCCCCGGTGGCACACACAGGCGACCGTAGCCCCGAACGGTTACGCCCCCGGACCC
74689 CTCATCCGAGACAAGGGTTCAGAACCGGTGCTGGGGCGGTACGTCCCCACACCTGGCGCAGGTGCCACAGACCTGCCCCACCGTGGCC
< • F R D S P R Y T G W V Q R L T G C V E G V T A
74780 CGGGCCCCGAGCGCTCTTCATCGGGTGCAGCACGTTCCCGGTACCCTCGGGCGGGCCCGCAGCTACCCAGCGCGGCTCGACGGCGTC
< R A R L A E K M P H L V N A T G E A A R L E G L A R E V A D
74872 GCTGTGCGCTCCACTCGCAGCTTGGCCAGCGCTCGGCCCTGGGCAGCCTCGATCGTCGGGTCCACCCGACGGGCTCGTACGGCTCGTCGG
< S D R E V R L K A L R E A Q A A E I T P D V R L P E Y P E D A
74964 CGTCGACCGTGAACCGTTGAGGCCGACCAACCGCTCGCCCGAGTCGATCTCCTGGGCGATCCGGTACGCGGACTGCTCGATCTCCCGC
< D V T F R N L G V V R E G S D I E Q A I R Y A S Q E I E R
75056 TTCTGGAAGCCGCTCGATGGCGTCGACCAGCGGTGGTCGGCCACCCGCTCCATCAGCTCCACCACCGCGCTCGATCTCGGCGGT
< K Q F G A E I A D V V S G H D A V R E M L E V V A A E I E A T

FIG.11A(65)

75148 CATCGCCTCCACCACGTACGACCCGGCGAACGGGTGCACGGTGGCGGTCAAGTCCGTCTCGTACGCGAGCACCTGCTGGGTGGCGCAGCGCCA
< M A E V V Y S G A F P D V T A T L D T T E Y A L V Q Q T R L A L
75240 GCCGGGGCGCCTTCTCGGTGGCGACGCGGATGGCCTCGTGAAGCTGTTCTGTGTAGCGACTGGGTGCCCGCCAGCACCGCGCCAGCCCC
< R A A K E T P L A I A E D F S N T H L S Q T G G L V A G L G
75332 TGGATCGCCACCCGACAGGTTACCTCGGGCTGCTGGGCGGTGAGCTGCACGCCCGCCGTCTGGGTGTGGAAGCGCAGCATCATCGACTT
< Q I A V R V L N V E P Q Q A T L Q V G A T Q T H F R L M S K
75424 CGGGTTCTTCGGCGCGAACTCGTCGGCATCAGCCGGGCCAGATCCGCCGGGGCGCACGGAACCTTCGCGACCTCCTCCAGCAGGGTGGTCC
< P N K A G F E D R M L R A Q I R R A A R F K A V E E L L T T R
75516 GGGCGACGAAGAAGACAGCCGGGGCGGAAGTCGTCCACGCCAGCCCGCGGCGAGCGCGCCGACGTACTCGACGCCGCTTGGCC
< A V F F F S L R P A F D D V A L G A A L A A R V Y E V G N A
75608 AGCGTGAACGGCATCTCTCGCGGGCGACGCGCGGCTCGGCCATGTGTAGCCGGAGATGGAGATGGTGTTCACACTTCGGCACCTCCCG
< L T F A I E Q A P S A G A E A M H Y G S I S I T N W K P V E A
75700 CCGGCAGTAGGCGAACGTGTGCGCGACACCGCGCAGCGAGGGCTTCGGCGGGAAGATGTACGTGCCCGGGCGATGTACTCCTTGAGGATGT
< R C Y A F T S A V L R L S P K P P F I Y T G R A I Y E K L I D
75792 CGTTCTGGATGTCGGTTCGAGCGCGCGCGCACCCCGCCTCCTCGGCGACGAGCTGGTAGAGCAGCAGCAGCACCGACCCCGGGGGG
< N Q I T G N L A A G P V G A E E A V L Q Y L L L V S G P A
75884 TTGATCGTCATCGAGGTGGAACCTTGTCCAACGGGATGCCGTGGAACAGCAGCCGATGTCCTCGATCGAGTCGATGGCGACGCGGACCTT
< N I T M S T S V K D L P I G H F L L R M D E I S D I A V G V K
75976 GCCGACCTCGCCGTGGCGATCGGGTCGTCGAGTCGTACCCCATCTGGGTGGCAGATCAAAAGCAGCGAGAGGCCCATGGTGCCGGCGC
< G V E G H A I P D D S D Y G M Q T P L D F A V S L G M T G A R
76068 GCAGGAGCTGGTAGCGCGCTTGTCTCCGTGCGGTGCCGAAGCCGGCTACTGGCGCATCTCCACGGCCGCGAGGTGTACATGGTG
< L L Q H Y R A N S E T A T G F G A Y Q R M T W P R S T Y M T
76160 GAGTAGACCCACGGGTGTACGGGAAC TCCCCCGGCTCGCCACGCCGCTCGGGCAGACCCTCCGGCAGGTCCCTCTGGGTGTAGACACCCCT
< S Y V G R T Y P F E G P E G L R E P L G E P L D R Q T Y V G K

FIG. 11A(66)

76252 GATCGGGAAGCCGGACTCGCTGACCGCGGTTCACTATCCCGGATGGTAGGACGTGCCACCGCGCGGAGGGTGAGGGATTGCGCACAT
 < I P F G S E S S R P E S M
 76343 CGCACCCCTGTCTTTCCCGCGGACTCGAGGGTGAACACCTGGCCACGTTCCGATTAGTTAAACGTTCCGCCGCGTGGGTTTCGCA
 76435 TCGGGGCTCGGAACCAAGATAGAGGAGTTGTGCCAGCCCCCTCGATTTCCCGGTGGCTCTTCTGTGACTCAGATCCGACGTGGA
 76527 GCGGGGACCAAGTCAGCCCCACCCACGGACGTGCGGCAGCCGGCACCATCGGTGACCGGTACTCGCTCCGGTCCGCGTGGGCAATGGC
 76619 GGCATGGGCACGGTCTGGCGTGCCACAGACACCCTGCTGCGGCGGACGTGGCGGTGAAGGAGGTGCTCTCCGCGCGGCCTCGCCCCGA
 > M G T V W R A T D T L L R R D V A V K E V V L P P G L A P
 76710 GCGACCGCAGCCCATGTACGAACGCACGCTGCGCGAGGCCCGCGCGGCGGCATCCAGCACCCGGCGGTGGTCCAGGTGTACGACGTG
 > S D R D A M Y E R T L R E A R A A A I Q H P A V V Q V Y S V
 76802 GTCACCGAGGGTGGTCGCCCCCTGGATCGTATGGAGCTGCTGGACGCCCGCAGCTGGCCGACATGGTGATCGAGGACGGCGCGGTGGCCCC
 > V T E G G R P W I V M E L L D A R S L A D M V I E D G P V A P
 76894 CCGCGCGGTGCCAAGATCGGCATGCCCTGCTCGGCGCGCTGGAGTGCGCCACGGCATCGGGGTGCTGCACCGCACGTGAAGCCGGCCA
 > R A V A K I G I A L L G A L E V A H A I G V L H R D V K P A
 76986 ACGTGTGATCTGCACCGACGGCGGTGCGTGCTGACCGACTTCGGGTGGCCAAAGTCCCCACCGACGTGCAGTCAACACGCCGGGGATG
 > N V L I C T D G R C V L T D F G V A K L P T D V Q L T T P G M
 77078 GTGCTCGGCTGCGCGCACTTCATCTCCCCGAGCGGGCCCATGGGCCAGGAGTTGCGGCCCGCCGAGCGACCTGTTCTCCCTCGGCGTCACGCT
 > V L G S P H F I S P E R A M G Q E F G P P S D L F S L G V T L
 77170 CTACACGGCGGTGAGGGCGGCCCCGTTGACAGGGGCGACCCGATCGAGACCATGCACGCCGTGGTCGAGGACCCGCGGCCACGCCGC
 > Y T A V E G R P P F D R G D P I E T M H A V V E D P P A T P
 77262 AGCGACGGCGCGGTGACCCGGGTGCTGATGGGGCTGCTGGAGAAGGACCCGGCCCGCGCTCGACGTGCACACCGCCGCGCGATGCTC
 > Q R S G P L T R V L M G L L E K D P A R R L D V H T A R A M L
 77354 CGCGAGTGTGCGCGGCGCGGTGACCAAGCACCGCCACCGCGTCAACTCGGTCAACCGACCCGTCACGGGTGTTGCCGTTCAAGCAGCGCCC
 > R E L L A G P L T S T A T A V N S V T D P Y A V V P V K Q R P

FIG.11A(67)

77446 GGCGTCGCCCCACGCGCCTCGGCTGCGGAGCCGAAGCCGAGCGGGCAGATCGGCGGGCGGCGATGCTGCCCCCGGCGAGTCGCTGACCG
> A V A P P S A A E P K P S G Q I G G R A M L A P G E S L T
77538 ACCGGCTGGCGGCCCTGCGCCGGGGCGAGAAGACGAGGAAGAGACGACCGCGCGCGCTGGACGACACCGCGCCGACGCGCTT
>D R L A A L R R G E K T R K R K T T A A A L D D T S A D A L
77630 GCGGGCCGCTGCACACCCACCGGGGCGATGCCGCGCCCCCGCGCGGCGGACGTACGGGGTTCTGCGGAGGCCACCCAGCGGGT
> A G P L H T P T G A M P A P P A G R T Y G S S E A T Q R V
77722 CGACGGGGACCGCGCGGAGGCCACCCAGCGGATGACGTACGGCAGCCCGCGCGACGCCACCCAGCGGTGTCCACGGGAGCGGCCCGT
> D A G T A P E A T Q R M T Y G S P P D A T Q R V S H G S G P
77814 CGGAGGCCACCCAGCGGTGCCCTACGGCGGCGGCTCGGCGGACGCCACCCAGCAGGTGCCCTTCGGTCGCGGCGCCGACGCGACGCGAGCGG
>S E A T Q R V P Y G G S A D A T Q Q V P F G R R P D A T Q R
77906 GTCCCTACGGCAGCCAGCCCGCGCGCAGCGCGGTCCCGGCTTCGGCGGTCGCGGACGCCACCCAGCGGTGCGCGGGCGTACGG
> V P Y G S Q P G A T Q P V P G F G A S P D A T Q R V G G A Y G
77998 CGGCGGCCAGTGTGCTGCCCGCACCGGCCAGCCGTGGGCCACCCCGCGCACCGCGCCGCCCGCGCCACCGCGCGCGGGGTGCG
> G G Q W S V P G T G Q P W A T P A T A P A P A T A G G G V
78090 GCCGCTCGTCGCCACGGTCAAGGGCTGGCCGCGCAAGTGCAGTCGCCGCGCGGCGGCGTCCCGTGTCTGCTGATCGGCGTGTTC
>G R L V A T V K G W P R K V Q L A A A G G V A V L L I G V F
78182 GCCCTCTTCGGCGGCGACGACCCGGAGCAGCCGACCCCGCAGGGGACCCGAGCGCGGGGCGCCCGCGCGCGGGTGGAGATGCA
> A L F G G D D P E Q P T T P Q G Q P S A G A P A G P G V E M Q
78274 GGAGCAGTCGGCCAAGGGCGTCACGGTGCAGGTGCCCCAAGGGCTGGGAGCGGCGCAGTGCAGCGGGCGTGTGGTTCGACTACATCGATC
> E Q S A K G V T V Q V P K G W E R R S A D G G V W V D Y I D
78366 CGGAGGACAACAGCCGCAAGGTGGCATCTCGCCGAGCGGTGGAGCGGACGTCGACGCGCTGGGCCGAGACCGCGCGCAACGGGCTGCGG
>P E D N S R K V R I L A E R W S G T S T R W A E T A A N G L R
78458 ACCCGTGGCCTCTGCCAGAAGCCGTACAACAGGTGTGATGACCGAGGAGTTCGACGGCAAGCGCGCGCGGAGTTCGAGTACAC
> T R S A S C Q K P Y N Q V S M T E Q E L D G K A A A E F E Y T

FIG.11A(68)

78550 CTGGGGCAGCGGAGGGCAAGCGGCACGGCGTGTGGCGGGGTGGTGCACGAGGGCAAGGTCTACTGTTCTACCTCTCCTCGACCGACG
> C G D G E G K R H G V W R G V V H E G K V Y S F Y L S S T D
78642 CCCGCTTCGCCGAGAGCAAGCCGATCTTCGATCAGATGGTGGCGTCGTTCAAGTCCGCGGGAGCGACTGAGCCGGGCGGGGGCCGACGC
>A R F A E S K P I F D Q M V A S F K L R G S D .
78733 GACGCGGCGGGCGGCACGCGACGTGGTAGCCGCGCGCTGCTATCAAGAGCCATGGCGGGGACACCACTGACCTCGACGACACG
> M A A D T T D L D D T
78824 CGCGATCTGGACGACCTTCGCGACCGGGCCCGGGGTGGCTCGACGACGACCCCGACCGGCCACCCGCGACGAGCTGGAGGCCGTGGTCGA
> R D L D L R D R A R R W L D D P D P A T R D E L E A V L D
78916 CGGGCTCGCGGAGCGGGCGAGCTGGCCGACCGGTTGCGCGGGCCACTGACCTTCGGCACCGCGGGGTGCGCGGCCCGCTGCGGCGCG
> G L P A S A A E L A D R F A G P L T F G T A G L R G P L R A
79008 GCCCAACGGGATGAACCTCGCCGTGGTACCCAGGCCGCCGGGTGCTGCGCTGGTCGCCGCCACAGGACGCCACCGGCCGCTGGTC
>G P N G M N L A V V T Q A A A G L V A W L A A Q D A T G P L V
79100 ATCGGGTACGACGCCCGGACGGCTCGCGGGAGTTCGCCGAGCGCACCCGCCAGGTGGCCACCGCGCGGGCGGCCGCGCTGCTGTGCC
> I G Y D A R H G S R E F A E R T A Q V A T G A G R P A L L L P
79192 CCGCCCCGTGCCACCCCGTGTGGCTACGGGTGCGGCAGCTCGACGCGGGCGCGGTGATGTTGACCGCCAGCCACACCCGCCCC
> R P L P T P V L A Y A V R Q L D A A A G V M V T A S H N P P
79284 AGGACAACGGCTACAAGGTCTACCTCGGCGCGCAGCTCGGCGGCGAGCTGGGCGGGGGCGCAGATCGTGCCGCCGCGACACCGGCATC
>Q D N G Y K V Y L G A Q L G G E L G A G A Q I V P P A D T G I
79284 AGGACAACGGCTACAAGGTCTACCTCGGCGCGCAGCTCGGCGGCGAGCTGGGCGGGGGCGCAGATCGTGCCGCCGCGACACCGGCATC
>Q D N G Y K V Y L G A Q L G G E L G A G A Q I V P P A D T G I
79376 GAGGCCGCCATCCGGGCGGTGCGGCCGTGCGCCGACGTACCGTGGGCCCGGCGGCGAGTCTGTCGGCGACGACGTGGTGTGCTGTACGT
> E A A I R A V G P L A D V P L G P A G Q V V G D V V V S Y V
79468 CGACCGGGCGCGCGTGGTCGACCCGGGGGCCCCGGAGCCTGAAGGTGGCCTACACGCCGCTGCACGGCGTGGGCGGCGCGCTGTA
> D R A A A V V D P A G P R S L K V A Y T P L H G V G A A V L

FIG.11A(69)

79560 CCGCGCCTTCGCCCGCGCCGGCTTCGGCATCCCCGGCGTGGTGCCCGAGCAGCGGTGCCGGACCCGGACTTCGGGACCGTCAGCTTCCCC
>T A A F A R A G F G I P G V V P E Q A V P D P D F R T V S F P
79652 AACCCGAGGAGCGGGGGCGGTGGACCTCCTCGTCGCGCTCGCCGAGCGCACCGGGGCGGACCTGGCGATCGCCAACGACCCCGACGCGGGA
>N P E E P G A V D L L V A L A E R T G A D L A I A N D P D A D
79744 CCGCTGCGCGGTGGCGTCCGCGACGGCCGGGGCGGCCCGGCACCGGTGAGTGGGGGCGCCTGGCGGATGCTGCGGGGACGAGGTGG
>R C A V A V R D G R A A G P A P V S G G A W R M L R G D E V
79836 GGGCGTGTCTGCCGACCATCTCATGCGCGTGGCTCCACGGCTGTACGCCACCACTGTGTCTGCTCCCTGCTACGGGCCATGTGC
>G A L L A D H L M R R G V H G L Y A T T I V S S L L R A M C
79928 GCCGCCGTGGCTGCCGTACGACGAGACGCTGACCGGCTTCAAGTGGATCGTCGGGGCGGCGGACCGCTGGGTGAGCGCGCTCCGA
>A A R G L P Y D E T L T G F K W I V R A G G P L G E A G S D
80020 CCCGCTGTCTTCGGCTACGAGGAGCGCTGGGCTACTGCTGCCCCGGAGCACGTCCGGCGACAAGGACGGCATCACCGCGCGCTGACCG
>P L V F G Y E E A L G Y C V A P E H V R D K D G I T A A L T
80112 TCGCCGAGCTGGCCCGCGGGCTGAAGGCGAGGGCGCACCTCACCGACCGGCTCGACGAGCTGGCCGCCGAGTTCGGCGTGCACCAACC
>V A E L A A G L K A Q G P T L T D R L D E L A A E F G V H H T
80204 GACCAACTCTCGGTGCGGTGGACGACCTGCGCATCATGCCGACGCGATGGCCCGGGTCCGGGGCGGCCACCCCGACGACCTGCTCGGCCG
>D Q L S V R V D D L R I I A D A M A R V R A A T P T T L L G R
80296 CCCGTTACCGAGGCGGGACCTGCTCCCCGAGGCGGACGTGGTGATCCTGCGTACCGACGGGGCACGGGTGGTGATCCGCCCGTCGGGCA
>P V T E A R D L L P E A D V V I L R T D G A R V V I R P S G
80388 CCGAGCCGAAGCTCAAGGCGTACCTGGAGGTGGTAGCCGGTGGCGGACGGCGACGTGCCGGGGCCCGGACGCGCGGGCCSCGCTG
>T E P K L K A Y L E V V E P V A D G D V P A A R T R A A T L
80480 GCGGCACTCCGCACGGAAATCGCCGCCCTGGTGCAGGGATGAGGTGTGCTCCCGCTTCGACGCTCTCTCAGCGGGTTGGCGTGTGCCCC
>A A L R T E I A A L V Q G .
80571 CAGGTTCTGGTGATATCGGGCCAGGTAAGCCACCCTCTGCCACTATCCATGCTGTAGAACATGATGCGTGCCACTTGGATGTAGTAGTAG
80663 GTGACCAATGAGGTGAACCCGGGGCCCTGTTTGAGCGTGTACGTAGCGCCGAAGCCACTGGCAGTCACATCGTCACGGGGGCTTCCCGTT

FIG.11A(70)

80755 AGCGCTCGGTAGCTAGCGCAGCAGGAACATCTCCCGCCATAGGGATACAGAGCTGGTGGTGTATCCCTTCTCGAAGGGCTTTGCAG
80847 GTTCTGCCGGAAGGGCGAGAGGTCTTGGGCTCCGTCTTGATCAGGATCTCGTAGAGCCGGACATCGGCCGTCTCGGTGTTGTACGCCAGG
80939 ATGACCGGCACCGGCAAGGTGTTGGGAGGGTGACCGAAATGGACGTGAACCCGGGTCGCGGGCGCTGCGTGGCCGCTGCCCGGCTTGGGT
81031 GCGGGGCCGTCGAGGAATAACTACGGAACATGCAACTGCCGTCTGTCTTGTGTACAGGAACAGCCACTGCCGCTTTCCACCCTCGCCGT
81123 TCACCTCGAAGGGCGCTACGGACGACCATCCAGCGCCCGAGTTGTCTTCTGGCCATCAGGGGCCACACCTGCTCGCAACCGTCTTCGTTG
81215 TCCACAACCTGCCACACGGCGCTGTTGCCGTAAGGGCATCGTAGAGCTGGACATACCGCTGTCTGCTGACGACGGAACGACGGAGGT
81307 CCACCCCTCCCGAAATTGCGCTGCCAGCGGGGAGGCCACTCGGGTGGCATCTCGTGTGGGCAATTGACTGGACCCGAAGCGGCCGTGCCGT
81399 CATTGCTGTTGTAGAACAGCACCGCTGGGCCACTGTAGTCCCCGTGAAATGCAGAGATATGACGTGCGTGAACCTGGTCCGAGTTGGACA
81491 TCATAGAGAGCATTCGGGAGTGACATGGGTTTACCCCGTCTAGGGATCACTGCTTCTCAACAAGATCATCAACGGTGTGCGGCAGGCTGCA
81583 CAATCGGGTGGAAAGAGCCAGCACCGGGCTCACTGGCCATCACAGTATCGTGTGACCTCTTCGACCGGGCCCGAAACGGGCGAACCGAG
81675 AGCGTTCGCGCATCTGTGCTCGGGCGTGTGAAAGGTGCGGCTGTTCCGCACGTGCGCGGGCAGCAGGGTGCCCTCCGCGCCGTACAGGGT
81767 TCTGCCACGAGGGCCAGGACCCAGACGGTGACCAAGCCGCCAGGGTGCCGGTCACGATGAACCGCTTGGCACCCTGGCTGCCCGCTC
81859 CGCGGGCCCTCCGCGCCGACCGGGAACGCGGCACGCTACCCCGCGTGATCCCTTGCCCCACGAAGGGCTCGTCTGAATAGCATCAGCACAT
81951 CAGGCCCCACCATTAACCGGCACCATTTGGCATTCGCTTTCTTCGACGTTGCGGTGCGGTGCCGGCGGTGTCATTTCCGGCGGAAAGGTGT
82043 TGCACGGTGCGTGAACAATGGCTCGACCGTGCCGCGACGGCAGCTCGGAGGCTGCTACCCAGCTCCGCGAGAGCGGCCCATATCAGCA

> V P R R Q L G R L L T Q L R E S A H I S
82134 TCGACGCGGGCGCGGAGCTGGACTGCTCGCGGCAGAAGCTCTGGCGGATCGAGCGGGGGCTGACCTCGGCCAAGACACCGGACGTCCGG

> I D A A A G E L D C S R Q K L W R I E R G L T S A K T P D V R
82226 GTGCTCTCGAGCTGTACCGGGCCACGCCGACCGGAGCGTGCTGCTCGGGCTCGCCGAGGTGAGCCGGGCCGAGGGGTGGTGGCACGC

> V L C E L Y R A T P D Q A S V L L G L A E V S R A E G W H A
82318 CCACGGCAGCTCCGTGCCGGCCTGTTCTCGCTCTACGTGCGCCTGGAGAACGTCCGAGCAGCATTCGGCACTACAACGGGAGCTGGTGC

> H G S S V P A W F S L Y V G L E N V A S S I R H Y N A E L V
82410 CGGGGCTGTGCAGACCCCGGCTACGCCACCGCGCTCTTCGAGCACAAACCGGCCGAGCTGGCGGAGGAGCGGAAAGGCGGTGGGC

> P G L L Q R P G Y A T A L F E H N R P E L G E E R K A V G

FIG.11A(71)

82502 TTCCGGACTCAGCGCAGGGGCTGCTGGCCCGGGGGTGCCTCCCGGCCCCGAGCTGACCGTGATCTCAGCGAGGCGGTGCTGCGCGGCCC
> F R T Q R Q G L L A R R L P P A P E L T V I L S E A V L R R P
82594 GGTGCGGGCGGATCGGTGATGGCCGACAGCTCCGGCACCTGCTGGCCGTGGCGAACGGCACAAATCACCAGTACGGGTGCTGCGCGCTGG
> V P G R S V M A D Q L R H L L A V G E R H N O T V R V L P L
82686 CCGCCGGGCGCGCTGGCCGCGAGGCGGCACGTTGCTGCTCGACTCCCGCTCTCGGGGCTCGGCAGCCCCGACCGAGCCGCGCGACC
> A A G P L A A E A G T F V L L D F P L S A L G S P T E P P T
82778 GTCTACGTCGAGGGGCTACCGGGCGGCTCTACCTCGACCAGCCGACGGAGATCGCCGCTACGAACGGGTCTGGAGGGTCTGGATTGCT
> V Y V E G L T G A L Y L D Q P T E I A A Y E R V W R G L D S L
82870 CGCCCTCGGCGCGCAATCAGCGGAGTGTGATGCCATCCGGGAGAGTGCTATGAGTGATCTGACCGGGCGCCGCTGGCGCACCCAG
> A L G A R Q S A E L I D A I R G E C Y E .
82961 CACCCGACGGCACCAACGGCGGGGACTGCGTGAGGTGGCCGACAACCTCACCGGCATCTGTCGGCTCCGGGACAGCAAGGACCCGGGCG
83053 GGCCGGCCCTGACCGTCCCGCCCGCCCTGGTCCGCCTTCGTACCGAGGTCAAGGCCAACCGCCTACCCGCTGACAGCTCCGCAACGAA
83145 CCAACCCCGGCTACGCCCTCAGACGGCGGCCAGGCCCGGCTGCCACGCCCTAGACAGCCCCGCGCTCAGACGTGCCTGCGCCTCAGAC
83237 AGCCCGGGCCGACGGGGCGGTGCGCCTCAGACGGCCCGGGCCTCAGGCGGCTTGCCGAGGGCGGCTCGACCGCCTTGCCCCAGGGCGGT
< . A R K G L A A D V A K G L A T
83328 GACGACCAGGGCCACCGAGGGGGGACCAACCGAGTGTCTCCAGGCTGACGGTGCCGGAGAGCCGGCCCCCGCGGATCTCTCCAGCCGAC
< V V L A V S P R V V S D D L S V T G S F G A G G A I E E L R R
83420 GCCGGGCTCGACGGCGGCTGCCGGTCAGGCCGAGCGCGGCTCCATCCGGAGCACCGCGACCAAGGTGGCCAGCGCCGCTGCGCCTCG
< R A D V A A D G T L G L A P E M R L V A V L T A L A A T A E
83512 TCGGGGATCTGCCCGCGCCAGCGCCTCGCCAGCCCGCGGGAGTCTCTCCACGGTGGCGTCCGCCGTGGGTAGCGGTGCACGTG
< D P I Q G G A L A E A L R R S D R R V T A D A T P Y R H V H
83604 GATGAAGCCAGCTCGGTCTCTCTGACGTGCGGCACCAACGCCCCGGGCGACCAAGGTCCGCCGAGGATCCGGTCCGCGAGGCGGTGGCGCAGCC
< I F G L E T E E V D R V V G R A V L D G L I R D R L G H R L R

FIG.11A(72)

83696 GCTGACCCAGGAGCGGGGTGTGGCGGTGTGGGGCCATCCGGCCAGGACCTCGTCCAGGATCGGTTCCCGGTGGCGCGGGGTCC
< Q V W S S P T H P T D A A M R G L V E D L I P E G T P A P D
83788 GTGACCACGAGTTCCCATCGACGTACGCGACCCGGCGGAGGGCCAGCTCGATCAGGACGGCGGGGCCATCCCGAGGTCGAGGCTGAT
< T V V L N G D V Y A V R G A L A L E I L V A A A M G L D L S I
83880 CCGCGCATGGTCGCCTTGCCGGATTGTCGTGTACGCGAGGAGCAGCAATTCTCGGCCAGGCGCAACACCGATCATGGCCGGAGACGG
< R P M
83970 TAGCGCTGAGCGCACCCCGTGGCGCCCAACTGCCCCACGAGCGCACTGCCCGGTGAGAGGGGAACCCGCTATACCGCAGCGGTTAACA
84062 GGGGGCCCTTCCTTCGATCAGAAGCGGGGCATACCGCCGAACCTGGCGGTGCCGGTCCCGGCGGACGATGAACATCCGGTCG
< . F R P M G G F Q R D G A D G L G P V I F M R D
84153 TTGAGGCTCTGTCGATCGCGGGGTGACGAGGCGCAGCGCAGCCGGACTGCTCCAGCCGGGCGATGCCAGCGGGCGGCGGAGCAGCA
< N L S E D I A A T V L R L P L G S Q E L R A I G V P A A L V C
84245 GAGCACGGTGATGTCGGTGCAGCCCCGCTCGGCCAGCAGCGGACAGTGCTCCAGGGAGCGCGCGGTGGCCAGCATCGGGTCGAGGACCA
< L V T I D T C G R E A L L R C C H E L S G G T A L M P D L V L
84337 GCACGGCAGCGCGGAGGTGCGCGGCAGCGACTCCATGTACGCGCGGCTCGTAGCTCTCTCTCGTCGCGGGCAGGCCGACGAAGCCC
< V P L G A L D R P L S E M Y A R P E Y T E D R A L G V F G
84429 ATGGACGACTCGGGGAGCAGGGCGAGCGCGGTGCGCCATGCCAGACCCGCCAGCACGGGTACCGAGCGGGGTGGCCAGCCG
< M S S E P L L A L A D A M G L G A R L V P V L L P N A L R
84521 GGTGCCCTCGGCGTCGGTGACGGGGTCTGCACCGGTACTTCTCAGCGGGAAGGAGCGGGCGGCCTCGTACCGAGCATGGTGGTGAGCT
< T G E A D T V P T Q V P Y K E V P F S R A A E Y V L M T T L E
84613 CGTGACGCGGCGGGAAGTTGGAGGAGTCGGTGC GCGGTCCCGCATGGCGGTGAGCCGCGACTGGGCGAGCGGATGGTCAATGACGTGT
< H L A A R F N S S D T R A S R M
84705 ACGTCCACGATGCCCCAACCTACCGAACGCCGGCCCCGAGACACGAGGAGCGACCGCGCTACCCGGCCCCGTGGGCAACCCCTGGACGGT
84797 TGGCGTTCGAAGGTAGGCGAGGTGCCCCAAGGTGGGGCCGACCTCGCCGCGTGATCAAGATCACGAGGCGTGGGGTCCGTAGACTTCCGGG
84889 CATGACGGCGACAGCGACGTGCGGCCCGGTGCGACCTCTCCGAGCTGGGACGATCCGAGACCGCTTTGCGGAACCTTCTGACGGCCTGCCG
> M T A T A T S A R S D L S E L G R S E T A L R N F L H G L P

FIG.11A(73)

84980 GGC GTG GAC CAG GTC GGC GCG GAG CAG CGG GCG GCG CCG CAG CTC GGC ACC CCG CTC GAT CAA GAC CAC GGC CAA GGC CCG GCG GAT CG ACCT GGC
> G V D Q V G A E Q R A A Q L G T R S I K T T A K A R A I S L A
85072 GAT CCG GAT GGT CG ACCT GAC CAC CCG TGG AGG GGG CCG GAC ACC CCG GCA AGT GCG GCG CTC GCG GCG CAA AGC ACT GCG CCG CCG AC CCG G
> I R M V D L T T L E G A D T P G K V R A L A A K A L R P D P
85164 CCG ACC CGT CCT GCG CGC CAG TCG CGC CAG TCT GCG TCT ACC CGG C GAT GGT CCG TAC GTG CGC GAG GTG CT GCG CGG AT CCG CGG GTCC
> A D P S C P H V G A V C V Y P A M V P Y V A E V L R G S A G S
85256 GGG CGG CCG TCC GCG GAC CCG GAC GGC AAC CGC GCG CCG GAC CCG GCG TGG TGC ACCT GGC CAG CGT GGC CAC CGG GTT CCG TCC GGG CA
> G R P S G G P D G N A P A G P G V V H L A S V A T A F P S G Q
85348 GGC ACC CCG TGG AGG TCA AGCT CGC CGC GAC ACC CGG CCG CAG TGG CGG CTGG CGG GAC GAG ATC GAC ATGG TGA TCA ACC GGG GCG GTTCC
> A P L E V K L A D T R A A V A A G A D E I D M V I N R G A F
85440 TGG CGG CCG CTA CCG CAG GTCT AC GAC GAG ATCG TGG CCA CCA AAG CGT GCG GGG AC GCG CCA CCT CA AGG TGA TCT GGA AAC CGGC
> L A G R Y R E V Y D E I V A T K Q A C G D A H L K V I L E T G
85532 GAG CTGG CCA CGTAC GACA ACCT GCG CGC GCG CTCT GGT GGC CATG CTGG CGG GCG GACTT CATCA AGAC CTG CAC GGC CAAG GTTCC
> E L A T Y D N V R R A S W L A M L A G G D F I K T S T G K V P
85624 CGT CGG GCG CAC CTTCC GGT GAC GCTGG TGA TGTGG AGG CGTCC GCG ACTTCC GCG CCG CCA CCG GCG GCG CAG GTCG GCG TGA AGCCGG
> V A A T L P V T L V M L E A V R D F R A A T G R Q V G V K P
85716 CCG CGG CATCA AGAAC CCA AGG CCG GATCA AGTAC CTGG TTAG GTCAAC GAG ACCG TCG GCG CCG GACTGG CTGG ACCCG GACTGG TTCTC
> A G G I K N T K D A I K Y L V M V N E T V G P D W L D P D W F
85808 CCG TTC GCG GCTCC AGCTGCTCAAC GACCTGCTCATG CAG CGCAC CAAGCTGAC GACCG GCGTCTACTCC GGTCCCG ACTACTTCA CCGCT
> R F G A S S L L N D L L M Q R T K L T T G V Y S G P D Y F T L
85900 GGA CTG AGCGTGA TCTTC GAATAC GCG CCG CCG GAGTCC CGCTCG GTGGTGG ACCTCAAG CCGCTCGTAC GGGCTGTTCTGTCGACGG
> D • > V I F E Y A P A P E S R S V V D L K P S Y G L F V D G
85989 GGA GTTCGTGAC CCGCG CAGCG GCGGCTTCAAGTCGGTCAAC CCGCGCTCC GAGGAGGTGCTCG CCGGAGATCG CCGAGGCGGCGCAGCG
> E F V D P A D G G G F K S V N P A S E E V L A E I A E A G S

FIG.11A(74)

86081 CCGACGTGGACGGGGCGGTCCGCGCCGCGGACGGCGTACGAGAAGGTGTGGGGCCCGATGCCGGCCGGGACCGGGCCAAGTACCTGTTCC
>A D V D R A V R A A R T A Y E K V W G P M P G R D R A K Y L F
86173 CGGATCGCCCGGATCATCCAGGAGCGCTCCCGGAGCTGGCCGTCTGGAGTCCCTGGACAACGGCAACCGATCCGGGAGTCCCGGGACGT
>R I A R I I Q E R S R E L A V L E S L D N G K P I R E S R D V
86265 CGACCTGCCGCTGGTCCGCGCGCACTTCTTCTACTACGCGGGCTGGGCAGACAAGCTGCCGTACGGGGCTTCGGCCCGAACCCTCCGGCCGC
> D L P L V A A H F F Y Y A G W A D K L P Y A G F G P N P R P
86357 TCGGCTGGCCGCGCAGGTCAATCCCGTGGAACCTCCGCTGCTCATGCTGCCTGGAAAGATGCCCCCGGCGCTGGCCGCGCAACACGGTG
>L G V A A Q V I P Q N F P L L M L A Q K I A P A L A A G N T V
86449 GTGCTCAAGCCGGCGGAGACCCCGCTGACCGCGCTGCTGTTGCCGAGATCTGCCAGAGCGCGAGCTGCCGGCCGGCGTGGTCAACAT
> V L K P A E T T P L T A L L F A E I C Q Q A E L P A G V V N I
86541 CGTACCGCGCGGGCGACACGGCGGGCGCTGGTCGAGCACCCGGCGTGGACAAGTTCGGCTTACC GGCTCGACCGAGGTGGCAAGG
> V T G A G D T G R A L V E H P G V D K V A F T G S T E V G K
86633 CCATCGCCCGTCCGTCGGGGCACCGGCAAGAAGTCAACCCTGGAGCTGGCGGCAAGGCGCGGAACATCGTCTTCGACGACGCCCGGTC
>A I A R S V A G T G K K V T L E L G G K A A N I V F D D A P V
86725 GACCAGCGGTGAGGGGATCGTCAACGGCATCTTCTCAACCAGGGGCACGTCTGCTGCCCGGGTCGCGGCTGCTGGTCCAGGAGTCGGT
> D Q A V E G I V N G I F F N Q G H V C C A G S E L L V Q W S V
86817 CGCCGAGCAGGTGCTGGAGTCGCTGAAGCGCCGAATGGCGTCTGCGGGTCGGCGACCCGTTGGACAAGAACACCGACATCGGGGCGATCA
> A E Q V L E S L K R R M A L L R V G D P L D K N T D I G A I
86909 ACTCGGCGCCAGCTCGCCCGCATCCGCGAGCTGTCCGCGCGGGCGAGGCCGAGGGGGCGGAGCGCTGGTCGCCCGCGTGGAGCTGCCC
>N S A A Q L A R I R E L S A A G E A E G A E R W S P P C E L P
87001 GAGCGGGGTTCTGTTTCGGCCGACGATCTTACGGGGGTCAACCAGCGCACCGGATCGCCCGGGAGGAGATCTTCGGTCCGGTGTGTC
> E R G F W F A P T I F T G V T Q A H R I A R E E I F G P V L S
87093 CGTGTGACCTTCGCGACCCCGCGAGCGCTGAGAAGGCCAACAACACGCCGTACGGGTGTGCGCGGGATCTGGACCGACAAGGGCT
> V L T F R T P A E A V E K A N N T P Y G L S A G I W T D K G

FIG.11A(75)

87185 CCCGGATCCTGTGGATGGCCGACCGGCTGCGCGCCGGGGTGGTGTGGGCCAACACGTTCAACAAGTTCGACCCGACCTGCGCGTTCGGCGGGG
>S R I L W M A D R L R A G V V W A N T F N K F D P T S P F G G
87277 TACAAGGAGTCGGGTACGGTCGCGAGGGCGGCGACGGGCTGGAGGGTACCTCGGTGCTGAGCGGGTCGCGGTACGCAAGACGTAC
>Y K E S G Y G R E G R H G L E G Y L G V .
87368 AAGCTCTTCATCGGCGGGAAGTTCCCGCGCAGCGAGTCGGGACGGTCGTATCTCGTGCATCCGCGAACGTGTCGCTGGCCTCCCGCAAG
>V Q S A N V S L A S R K
87458 GACGCGCGGACGCCGTGGTCGCGCGCCCGCGCGCGTGAAGGGCTGGCGCGGGCGACCGGTACAACCGGGTACAGATCCTTACCGGGT
>D A R D A V V A A R A A V K G W A G A T A Y N R G Q I L Y R V
87550 CGCCGAGATGCTGGAGGGCGCGCGAGCAGTTCGTGCGCTCGGCGTCCGCGCGACGAGGTCGACGCGCGATCGACCGTGGGTCTGGT
>A E M L E G R R E Q F V A L G V P A D E V D A A I D R W V W
87642 ACGCGGGCTGGTCCGACAAGTCCCCAGGTGTACGGCGGTGCGAACCTGTGCGCGGGCCGTACTTCAACCTGTCCGCGCCGAGCCGACG
>Y A G W S D K L P Q V Y G G A N P V A G P Y F N L S A P E P T
87734 GGGTGGTGGCCGTGGTGGCCCCGAGGCCCCCGCGTCTCGGCTGGTCAGCGTGATCGCCCCGGCGATCGTCACCGGCAACACGGTGGT
>G V V A V V A P E A P A L L G L V S V I A P A I V T G N T V V
87826 GGTGGCGGCTCGCCGACCCAGCCCTGGCTGGCTGACCTGGCCGAGGTGCTGGCCACCTCCGACCTGCCCGGGGGTGGTCAACGTCC
>V A A S P T Q P L A S V T L A E V L A T S D L P G G V V N V
87918 TGACCGGTCCGATCACCGAGACGGTGCCGACGCTCGCGGCGCACCTGGACGTCAACGGCATCGACCTGACCGGGTGGCGGACGCGTCGCTC
>L T G A I T E T V P T L A A H L D V N A I D L T G V G F A S L
88010 GCCACCGAGCTGGAGGTACAGGCGGCGGAGAACCTCAAGCGGGTGATTGCGCGGGCCCCGGCCGACCACTGGTACGCGGACCCGGGCGCT
>A T E L E V R A A E N L K R V I R P A P A D H D W Y A D P G L
88102 CACCCGGATGACGACGCTGTGGAGACGAAGCGTCTGGCACCCCAAGGGCGTCTGAGCCCAACCGCCGTCACCGACCCCGCCGCCAC
>T R M T T L L E T K T V W H P K G V .
88193 CCGGCGCGGAGGCAGGGGTGGGCGGGGTGGGTGGATCTACTACGAGGGGTAGGATTGCCCGGTGACTCGGTGGGTGATCTTGAGC

FIG.11A(76)

88284 GGGCGGTGATGGACGTGCTGTGGGACACCGTCCCGGGACAGTCGGACGGGTGACGGTGCGCGAGGTGCGCGAGGCCCTCGACGGCCGCGA
> M D V L W D T V P G T S D G V T V R E V A E A L D G R E
88375 GCTGGCGTACACGACGGTGATACCGTGCTGGACCGGCTCGCCGGCAAGGGCATGGTGGGCGCCAGCGGGAGGGCGGGCCTGGCGCTACC
> L A Y T T V M T V L D R L A G K G M V R R Q R E G R A Q R Y
88467 AGGCGCGGCCAGCGCGAGGGCGACATCGCCAGCTCATGCTCGACGGCTGGACCTCGGCGGACGCCGGACGCCGCTGGTGGCTTC
> Q A A A S R E A H I A Q L M L D A L D L G G S R D A A L V R F
88559 GCCCGTGGTGACCGGACCGAGGCCGAGGTGCTGGCGCCGCCCTCGGCGCCGAGCGGGCGGCCCGCTGACCGACCGGTCGACGGCC
> A R S V T G T E A E V L R A A L G A E A G G P L T D R V D A P
88651 GCGCGCGACCGGGCGGGCAGCCGCCCTGGCCGACGAGCGACGGACCGGTAGGGCCGCCGTATGGCGTACGCCGTGCACTTCGCCG
> R A D R A G Q P A L A D E A T D R . > M A Y A V H F A
88741 CGACGGTCTGGCCTGTACCTGACCGTCAAGTCTTGGCGGCTCCACCTGGACGTGGCGGGCCCCCGGATCGCGATCGTCTGCTGGCAG
> A T V L A C Y L T A Q V L A A S T W T W R A P R I A I V C W Q
88833 GCGGTCGGGCTCGGCTCGGCTCTCCGCGATGGGCTGCGGCTGGCGGTACGACCGGCCGACCGCGCGGCGTTGCT
> A V G L A L G L S A M G L P M A L G V A A Y D R P T G S A L L
88925 CGCCCTGGCCACCGACCTGACCCACGGCACCCCTGCCGGCGGGCTCGGCGGGTCCACCTCGGTGTTGGGTGGGTTCGGCATCGGGG
> A L A T D L T H G T L P A G L G A V H L G L V G G F G I G
89017 CGGCGTGTGCCACGACGGTACGACGGTGCAGGCGACCGTCCGGGCCAGCGGCAGCACCGGGACCTGCTCGCCCTGGTGGCCCGGCGG
> A A L L A T T V R S V Q A T V R A Q R Q H R D L L A L V A R R
89109 GACCCGAGGTGCCGGGGCGTGGTGTGGACCATCCGAGCGGGCGGTACTGCCTGCCGGGCGTGGCGCCCGGGTGGTGGTCAAGCGC
> D P E V P G A L V L D H P S A A A Y C L P G V R P R V V S A
89201 CGGGCGCTCAGCATGTTCGACCGGGCGAGTGGCGGGTGTGACCCACGAGCGGGCGCACGCCAGGAGCGCCACGACCTTGTGCTGC
> G A L S M L D R A E L A A V L T H E R A H A Q E R H D L V L
89293 TGCCGTTACCGGCTGTGCCGTGCGCTGCCCTGGTTCGGTGGGTACGCGACGCGCGGCTGCCCTGCTGGTTCGAGATGCGCGCC
> L P F T A L C R A L P W F R W V R D A H E R V A L L V E M R A

FIG 11A(77)

89385 GACGACAAGGCCGGGAGCTGCACCCGAGGCTCCCTCGCGGGGGCGTTGCGCCGGTTGCGCGCGCGGCCACCGGATCGCGCCGGCCGG
> D D K A R E L H A E A P L A G A L R R G A A A G H R I A P A G
89477 CACCCTCGGCCTGGCGACCGGGACCTGGACGTCCGGGTCCAGCGGCTGCTGGTCGCCGACCGCGCGCCCGCGGTGATCGGGGCGCGCGCGC
> T L G L G D R D L D V R V Q R L L V A D R P P R L I G A A A
89569 TGGCGGTGGCGGTACCCCTGGTCGCGCTGCCGGTCTCCCTCTTCTGAGCTGACGCCCGACCCGGACACGTCCGACCCGGACACGCGCGGAC
> L A V A V T L V A L P V S L F L S .
89660 CGGACACGTCCGACCCGGACGCCCTGCCCCGAGTTGGGCCGTTGCCACGGGGCGGCTGCGCTGCCGTTGCCGGGCCACCGACATGCGGG
89752 GCGATAGGTAGAGCCTACGTGTAGTCTTCTACGACAAGGGAGCCTACTACCGAGGGCGGCCATGGATCAACTGCTCCTCGCCCGTC
> M D Q L L L A R
89842 TCCAGTTCGCCACGACCACCTCGCTGCACTTCTCTTCTGTCGTGTCACGCTCGGTCTGGTCAACCTGCTCGTGGGCTCCAGACGGCCTGG
> L Q F A T T T S L H F L F V V T L G L V T L L V G L Q T A W
89934 ACGATCACCGGCAATCCCGTCCACGAGCGGCTGACCCGGTTCTGGGGTCAGTCTACGTGATCAACTACGTGCTCGGCATCGCCACCGGCCT
> T I T G N P V H E R L T R F W G Q L T V I N T V L G I A T G L
90026 GCTCATGGAGTTCAGTTCGGGCTGAACCTGGAGCGGCTGTGCGCTACGTGGCAACGCTCTTCGGCGCCCGCTGGCGATCGAGACCCCTGG
> L M E F Q F G L N W S G L S R Y V G N V F G A P L A I R T L
90118 TCGCGTCTTCTGGAGTCCACGTTCTCTCGGGATGTGGATCTTCGGCTGGCACCGGCTGCGCGGGGCGTGACCTCGCGTGTGTGGGC
> V A F F L E S T F L G M W I F G W H R L R R G V H L A L L W G
90210 GTGGCGCTGACCGCGTACGCCCTCGGCGTTCTGGGTGATGGTGGCGAACGCTGGCTGGCTGCAGAACCCCGTGGCTACGAGGTGCGCGACGGGT
> V A L T A Y A S A F W V M V A N A W L Q N P V G Y E V R D G V
90302 GGGCCACCTGACCGACTTCGGCGCGTGTGCTGACCAATCCACCTTCGGCTGGCCTTCGGGCACGTGGTGGCGCGCCCTGCTACCGCGCG
> A H L T D F G A L L T N P T F G L A F G H V V A A L L T G
90394 GGATGCTGATGGCGCGGTGAGCGCTGGCACCTGATCCGGCGCACCCCGGACCGGCTGTTCGCGACGTGCTGCGGATCGGCCTGGTC
> G M L M A A V S A W H L I R R T P D H A L F R T S L R I G L V
90486 ACCGCGGGGCTCTGATCAGCCTGGTGCAGGGCTTCGCCCTTCGCCAGTTCCGGGCGGTCGGGCAGACGACGCCACCAAGTTCGGCGCGCG
> T A A V S I S L V Q G F G F A Q F G P V G Q T Q P T K F G G G

FIG.11A(78)

90578 CGCGCAGCGGACGCCCTGGTCGCCGAATGGACCTCCCGGTTCCGGGCCGGGCGGACTACACCCGCCCGTGTGTCGCCGACGTGGGCTCGGTT
 > A Q R D A L V A E W T S R F G P G D Y T P P V L A D V G L G
 90670 TCAATGATCTGATCGGCCCTCCTCTGGGCTGTCTGTGGCTGTCTGCCCTGCTCTGGCGGACTGGTTTCATCCGGCTGCGCTTCCCGCTC
 > F M I L I G L L L G C L W L L L P L L W R D W F I R L R F P L
 90762 TGGCTGATCCTGTGTCGGCTGCCCTTCTGTCGGGTGATCCTCGGCTGGATCGCCCGTGAAGTGGGCCGCCAGCCCTGGGTGCGGTA
 > W L I L L A L P L P F V A V I L G W I A R E V G R Q P W V A Y
 90854 CGGGCTGCTTCCACCGAGCGGGGGTCTCGCCGGTCCGCCCGGGGTGATGCTCGCCTCGCTGATCGGCTTACCCCTGCTGCTCGGGGGGC
 > G L L S T E R A V S P V A P G V M L A S L I G F T L L L G G
 90946 TCGCCGTGCGCAACTGGGTGCTGTTGCCCCGGTACGCCGCCCGGGGAGCGCGGATCCCGCCCTAGGCCGCCCGGCCCGCCAGCCGCGGAC
 > L A V A N W V L F A R Y A A R G A A D P A L G R R P G P A A D
 91038 GAGTCCCGTCCCGTCCCGTCTCGGCTGAGGAGGCCCTGTGGAACCTGCGCTGATCGCCCTGCTCGGGCTCTTCTCGCCGGCTACC
 > E S R P V P L G . > V E L A W Y A L L G L F L A G Y
 91127 TGGTCTCGGGCGGTACGACTACGGCGTGGCCTGCTGCTCGCCGGGGGGCCCGCCGCCGCCCGCCGCCCGGCCCTACCGCGGTGGGC
 > L V L G G Y D Y G V G L L L A R G G P P A R R A A L T A V G
 91219 CCGTCTTCTCGGCAACGAGGTCTGGCTGGTGGCACCCTGCGCATTCGTTCGGCGCGTTCCCCACCCTGGAGGGGAACCTGCTGTCCGG
 > P F F L G N E V W L V A T V G I L F G A F P T L E G E L L S G
 91311 CTTCTACCCCGTCTGCCCGCCGCGCTGGCCGGGTGATCATGTTGACCGTGGCGTGCAACTGCGCAGCCGCCCGACGAGCGGACCC
 > F Y P V V A A A L A G V I M V T V G V Q L R S R P T D E P T
 91403 GCGCCGCTGGGACCGGATGGTGGCCGCCGGGAGCCTGCTCGCCGCGTTCCGGCTGGGGGGCGCTGCTCGCCGGGCTGCTCCAGGGCGTACCG
 > R A A W D R M V A A G S L L A A F G W G A L L A G L L Q G V P
 91495 CTGGCCGCGACGGCACGTACGGGCGTGGCCACCGTGGCCACCCCGTTCCGGGCCCTCGCCGGGCTGGCGATGACGGCCCTGGTGGCGGT
 > L A A D G H V T G V G H V A T P F A A L A G L A M T A L V A V
 91587 GCACGGTGCAGCTTCTACGCTCCGGCTGTGTGGCCGCCGACCGCGCACCGTGGCGTACCGCCCGCGGCTGGTGGCGGTGGCGCTCG
 > H G A T F L T L R L S A A D A A P L A R T A R R L V A V A L

FIG.11A(79)

91679 CCGCCGTGCCCGCGCTCGCGGGCGGCTCTCCGATCGGGTACGCGCGGACGCGCCGCTGCCGGCGGTACTGTCGCCGTTG
 >A A V A L A A V A G A L S D R V R A A R Q R P L P A V L L P L
 91771 GTACTGGTGGCGGCTGCTGGTGGCCGGGCGGCACGCGCGGACCTGCCCCGGGTGGCTTCGCCGCCACTTCGGCGGCGCTGGCGCT
 >V L V A A L L V A R A A H A R H L P G V A F A A T S A A L A L
 91863 GCCGGTGGCGGAGTCGGCGCGGCTGTGGCCCTACGCGCTGGTCTCCACCGTCGCACCGACGCGCATCACTAGCGGTGACCGACGCGGCGG
 >P V A G V G A A L W P Y A L V S T V A P T A S L S V T D A A
 91955 CCAGCGGGCCGACGCTGACGGTGTGGGTGGCTACCGCTCCTGCGGGCCCTACTAGGCTTCCAGGCGATGTGCTGGGTGTTT
 >A S G P T L T V L G W L A L P L L P A L L G F Q A M C W W V F
 92047 CGGGACGAACCGACGGCAGGCGACCGGTGTACTGGTAGCGCGCTCCCTTCGACCCACGTCTGCTCCGCCGGGTCCCCGCGGCCCCGGCG
 >R G R T D G R A P V Y W .
 92138 CGACCTCGCGGTGCTCGCGGGGTGACGGCGCTGGTGGTGGGAGGCCACGCGCTGGCCACGGTGTGGCCGCGCG
 >V L A V L G G L T A L L V V G Q A T A L A T V L A A
 92229 CTCGACGGCGGTGGCCCCGGCGGCTCGCCGGTTCTGGCCCGCTGGTGGGGGGGCGCTGGTCGCCTGGGCCACGGTGGC
 >L D G R L A R P A L A G F L A A V V G R A L V A W A Q G T V A
 92321 GGCGCGGCGCGGACGGTCAAGCGGCGCTGCGGGCGGACCTGCTCGCGCGCTGGCGCGGACGGTCCCGGTGGTGGCGGCGAGC
 >A R A A A T V K A A L R A D L L A A V G R H G P G W V A G Q
 92413 GGGCGGGCAGCTCGCCACCCTGGCCGGGGGGGTGGACGCCCTGGACGCTACTTCACCGGGTACCTTCGCGAGCTCGTGTGTCAGCGTC
 >R A G Q L A T L A G R G L D A L D A Y F T G Y L P Q L V L S V
 92505 ACCGTCCCGGTGGCGGTGCTGGCCGGATCACCTTCGCCGACTGGGGCTCGGGCGTCATCGTCGCGCTGACCTGCCGCTGATCCCGGTCTT
 >T V P V A V L A R I T F A D W G S A V I V A L T L P L I P V F
 92597 CGGGCGCTGCTCGGTGGCAGGCGAGCGCCGCCACCGAGCGGAGTGGCGGGCGGTGTCGACGCTCGGGGGCACCTTCCTCGACATGGTCG
 >G A L L G W Q A Q A A T E R Q W R R L S T L G G H F L D M V
 92689 CCGGCCTGCCCGCGCTCGGCCGGGGCCGAGGTGAGGTGGTCCGCCGGATGGCCGAACGGGACCGCGCGCGGACGATG
 >A G L P R L R A F G R A R G Q V E V V R R M A D G H R A A T M

FIG.11A(80)

92781 CGCACGCTGGGATCGGTTCTGTCCGGCTGGTGTGGAGCTGGTCGCCACCTGTCTGGTGGCGTGGTCGGGTGCCGTGGGCATCCG
 > R T L R I A F L S A L V L E L V A T L S V A L V A V P V G I R
 92873 GCTGCTGGCGGGGCTGGCGCTGTCCACCGGCTGTGGTGTCTGCTACCCCGAGGCGTACCTGCCGCTGGGGCGGCGGAGCC
 > L L G G L A L S T A L L V L L L T P E A Y L P L R A A G S
 92965 GGTTCACGCCAGCATGGAGGGCTGGCCGCGCTGGACGAGGCACTGACCTCTCCGCCGCCGACCCGACCCACGGCCACCGCGGGTCTG
 > R F H A S M E G L A A L D E A L T L S A A D P T A T A T A G S
 93057 CGGCCCGTCCCGACGGGCGCGGATCCGGTCGAGGGCCGTGACCGTACGAGCGGACCGTGGCGCTACGGGACGTACGCTGAC
 > R P V P D G R A E I P F E G V T V A Y E R T V A L R D V T L T
 93149 AATCCGGCCCGGAGCGGATCGCGATCGTGGGCCGAGCGGCGGGCAAGAGCACCTGCTAACCTGCTCGGCTTCGTGCCCCCGA
 > I R P G E R I A I V G P S G A G K S T L L N L L G F V A P
 93241 CGCAGGGCCGGTCAACGTGGTGGCTCGACCTGGCCGCGGACCCGACGGTGGCGGCTAGGTCCGCTGGTGCCGCAACGGGCC
 > T Q G R V T V G G V D L A G A D P D G W R Q V A W V P Q R A
 93333 CACCTCTTCGGCGCCTCGCTGACCGACAACATCCGGTCCGTCGCGCCCGGACGCCGCGCTCGCCGGCGGCTCGCCGCCCGC
 > H L F A A S L T D N I R L G A P G T P D A A L A G A V A A A
 93425 GCTGGACGAGGTGTCGCCGCCCTGCCGACGGGCTCGACACCGTGTCTGGTGAGCGGGGACGGCCTGTCCAGCGCCAGCGGCGGG
 > L D E V V A A L P D G L D T V L G E R G H G L S S G Q R R
 93517 TCGCCCTGGCCCGGCGTTCCTGCGGGACGCGCGGTGGTGTCTGGACGAGCCGACCGCGGGCTGGACACCGCCAGCGAGCGGGGTG
 > V A L A R A F L R D A P V V L L D E P T A R L D T A S E A G V
 93609 CTGGCCGCCACCCGCGGCTGTGCGCGGGGGAACCGCCCTGTTGGTGGCCACCGGCGGCGTGTCTCCGACGCCGACCGGATCCTGCG
 > L A A T R R L V A G R T A L L V A H R P A L L S D A D R I L R
 93701 GGTGAGGAAGCGGGTCACCGAGCTGACCACCCCGCCACAGGGGTGACCCCGGCCCGGCGAGGGGCTGCCGACCGCGGGC
 > V E E G R V T E L T T P A T G V T P G P G E A A A G P A G

FIG.11A(81)

93793 AGGTGCCCCCGCCGGAGAGGGGGCCGATGAGACCGGTCCCGCCGACGACGCCTTCCGCCATCCCGCTGCCGGCCGACGGG
 >Q V A P A P A G E G A A R .
 > M S T G P A D D A F A I P L O A D G
 93884 GCCCCGTGGCCGGCAGCTCCGGGCGCCGAGGGCCGTGCTCCGGCTGGCCCGCGGTACCTGGGCCGGCTGGTCGGCGCGGGTCT
 > A P V A G G S V R A A E R A V L R L A R P Y L G R L V G A G L
 93976 GCTCGCCGCGCCACCGAGTTCCGCGGCTGGCCCTGATGGCCACCGCACCTGGCTGCTGATGAGCGCCCGCGTGGCCACCACTGGACC
 > L A A A T E F A G L A L M A T A T W L L M S A A G R P P L D
 94068 GGCTACCGTGGCGATCGTCGGGTCCGGGCGCTGGCGATCAGCGAGGCGTTCGCTACACGAGCGCCTGCGCGGCCACGATGCCGTG
 > R L T V A I V A V R A L A I S R G V F R Y T E R L A G H D A V
 94160 CTGCGGATGATCACCGACGTCCGGGCGGGGTCTTCGCCGCCCTGGCCGCCGCGGCGACGCCGCCGAGCGCACCGGGGACGCGTGAG
 > L R M I T D V R A G V F A A L A A R R D A A R Q R T G D A L S
 94252 CCGGCTCGTCCGACGTGGAGCCGTGCAGGACCTGCTGCGGGTCTGTCGCCGGGGCGCGCCACGGTGGTGACGCTGTGGCCG
 > R L V S D V E A V Q D L L L R V L V P G A A A T V V S V L A
 94344 TGGCCGGGGCCACCACCATCTCGTCCCCCGCCGGGTGCTGGCGCTGGGCGCTGCTCGCCGGGGTGGCCCTGCCGTCGCGGCCACC
 > V A G A T T I S L P A A G V L A L G L L V A G V A L P L A A T
 94436 GCGTGACCCGGCACGCCGCGGTGGCCCGCTGCGGGCGGCTGCGCCACGGACGCCGTGGACCTTGTCACGGCGCCGCGACCT
 > A L T R H A A D R V A P L R G A L A R D A V D L V H G A A D L
 94528 GGCCGCGTTCGGTGCCACCGGTACGCGCTGGACGCCGCCCGATCGGGCCCGCGGCTGGCCCGGCTGGAACGACGGCTGCCGCCACCG
 > A A F G A T G Y A L D A A A D R A R R L A R L E R R L A A T
 94620 GCTTCGCCGTGGACGCCCGGGGCGCTCGTCCCGGGGTGACCGCGGACGGTGCTGGTGCTACCGCGCTGCGCGACGGCTGGCGGGGTG
 > G F A V D A A G A L V A G V T A G T V V V T A L R D G V G V
 94712 CTGGTCGGGTGCTGGCGTCCCTGGCCGCGCTCAGGTGGCGCTGGCGCTGGTGGGGCCGCCGAGCGCACCCAGCTCCGGGC
 > L V G V L A V G S L A A V E V A L A L V G A A R Q R T R L F A
 94804 CGGGCTGGTCCGGTGGCCGCTGTGACCGCCCCGAGGCCGACGCGCCCGCGCCACCCCGCGGTGCCGCCGCTGCCGCCGCGCTCG
 > G L V R V A A L L T A P Q A D A P A A T P P G A A R A A V

FIG.11A(82)

94896 GTCCGCGCCGACGAGTGGCTTCGACGCGGTACCGTGGGTACCGGGCCGGCACCGCCCCGGCCCTGGACCGGGTCACCCCTGGACCTG
 >G A G P H D V R G D A V T V R Y R A G T A P A L D R V T L D L
 94988 CCGGCGGCGCGGGTGCCTGGTGGGGCCGAGCGGCGCCGGAAGAGCACCTCGCCGCCGTCTCACCGGCACGGTGCACCCGAGCA
 >P A G R R V A V V G P S G A G K S T L A A V L T G T V R P E Q
 95080 GGGCCGGTCAACCTCGACGGGGCCGACCTGTGGCGTACCCGGTCCGAGGAACCTGCCCGGGCCGTGGCGGCCCTGCTGCCGAGGCGGTACG
 > G R V T L D G A D L S A Y P V E E L P R A V G G L L A E A Y
 95172 TCTTCCACGCCAGGTCCGGGAGAACCTGCTGCTGGCCGGCCCGCCGACGAGGGGAGCTGACCGCCGCGACCCCGGGCGGCCCTG
 >V F H A T V R E N L L L G R P A A D E A E L T A A T R A A G L
 95264 CTGGACTGGGTGCACGCCAGCCGGCCGGTGGGACACCGTGGTCGGCGAGGAGGGCGGACAGCTCTCCGGCGGCCAGCGGACGCTCGC
 >L D W V H A Q P A G W D T V V G E E G G Q L S G G Q R Q R L A
 95356 GCTGGCCCGGGCGCTGCTGCGCGCGCCGGGTGCTGGTGTCTGACGAGCCGACCGAGGGGCTCGACCCGTCGCGCCGCGACGCGGTGCTCG
 > L A R A L L A A P G V L V L D E P T E G L D P S A A D A V L
 95448 CCTCGGCGTGGCGGCGACCCCGCGGCACTCGGTGCTGTGATCAGCCACCGGCTCAGCGGGCTCGCCGACCTCGACGAGATCGTGGTG
 >A S A L A A T P A G H S V L L I S H R L S G L A D L D E I V V
 95540 CTCGACGCGCGGGTGGTCCAGCTGGCCGGCACGACGAGTTGGTCGCGCGCGGGGCTGGTACCGGGACCAAGTGGTGTCTCCAGGAGGC
 >L D A G R V V Q E G R H D E L V A A P G W Y R D Q W L L Q E A
 95632 GGCCGAGCGGGTACCTGGCCCTGACGCCCCGCCCTGAGCCGGCTCCGGGATTCCCCCGACCGCTCGGCAGTCACCGCATGGCAGGCT
 > A E R G Y L A L T P R P .
 95723 CGTCGCATGGTGGCTGCGACGACGTACTCGTGAAGGAGCGGCTGCGCGAGTTGAGCGACCGGCTGCACGGCCCGGCACGGCTCAAGGCCG
 >M V R C D D V L V K E R L R E L S D R L H G P A R L K A
 95814 ACCTGTGGCCGAGGCCCGCCACGCGTTGCAGGACGCCGTGAGGCGTACCGGGACGGCGGGGCTGCCGGCGGAGGCGGAGCGGGGCA
 >D L L A E A R H A L Q D A V E A Y R D G G L P A A E A E R R A
 95906 GTGGCCGAGTTCGGCGAGCCGCCGGCTCGCCCGCGGTACCAAGCGGGAGCTGGCGGGCGGGTGTGCTGCGGGGCTGTCCCTGCGGGTGTCT
 >V A E F G E P A R L A P A Y Q A E L A A G S L R G L S L R V L

FIG.11A(83)

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95998 CGCGGTCCGGCGTCTGGTCTGCGGGCGATCTGACCTGGCAGGGGTGAGCTGGAGCGGGCCCCGGCCCGCGCGGCGCTACCGCC
    > A V A G V L V V A G D L T W Q G S S W S G G P P A A Y R
96090 TGTGTCCGCTCGGTGGACGGCATCTGGCTGGGCGGGTCTGCTGTGCTGGCGGGTTGCTGTGTCGCCGCTCGGCCCGGTGGGCG
    > L L S A S V D G I W L G A V V L S V A G L L L V A A S A R W A
96182 CACCCGGCCCTGCCCGGCTGCCCGGCTGACCGGTCTCGGGCTCACCGCACGCTCGTCTGGGCGTGGCGACCGGCGGCCCTGTACGC
    > H P A L P R L A R L T G L G L T A T L V L G V A T G A A L Y A
96274 CTGGTCGATCGGGCTCTGGGAGGCGGCCGACCTGGCCGCGATGCTGTGGGCGGCTGGTCTGCGGCGGGGTTCTTCTGGATCGGTC
    > W S I G L W E A A R T W P P M L V G A L V C G A G F F W I G
                                     junction
marker
96366 GGGCGGCCCGGTCTGGTGTCTCTGGCAGCCGACCGCGGACCGGCGTAGTCGGGTGGCGGGCGCGGTAGGCCGGCGTGGCGG
    > R A A R S W L L S A R R P A G P A .                                     < . A P T A P
96457 GGGTGTCCCGAGGAAC TGGCCGACGGTGC GGTGA ACTCCCGCAGCGGCGCGTTC CCGGCGAGGGCCCCGGCGCGGAGTCGGTCAGC
    < T D G L F Q G V T A S F E R W G A R E G A L A R R G S D T L
96549 TCGTAGGTCCGGCGCTCGCGGCGGTGACGGTGTCCA ACTGTGACCACTGCCCCGCCGCTCCAGCCGGCGCAGCGCGGTAGATCGT
    < E Y T R R E R G N V T S W S S V V H G A R E L R L A P Y I T
96641 CCCGGTAGGCAGATCGAGGCTGCCCTCGCTGCGCGCGCGCAGCGCTCGATGATGGCGTAGCCGTGACGGCGGCCCGCTTCCAGCACCCGGA
    < G T P L D L S G E S R A R L A E I I A Y G H L A G R E L V A L
96733 GCAGCAGCGCTCGAGGTGTCCGTGCAGCGCCTGGGCGCTTCATAGGTAGCAAGACTACTTGTGGGCCACTCGCGCGGCCACCGGGGTGCGG
    < L L A D L H G H L A Q A K M
96824 GCACCGGGCCTCCTAAGCCGCCCACTAGGGTATGTGCCCCAGAGTCAC TCGGGCGCGGAGACGCGCGCGGTGGGCAGCCCCGAAGCACAC
                                     > V G S P K H T
96914 GGAGGTCAGGTGGCCCGCCAGTCGCCCCCAACGGCCCCGACGCCGAGCCTGAGCTCGACGAGACCGACGGCACCGCGCGCAGAGGTCGAAG
    > E V S V A R Q S P Q R P D A D E P E L D E T D G T A A E V E

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FIG.11A(84)

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97006 AGGACGGCGCGCCGTCGGCGCAGGACGCCGCGCTCTGGGACGAGCTGGCATCGACCCGGTCGAGATCGCCCTGCCCGCCGGC
    >E D G A R P S A Q D A D R A L W D E L R I D P V E I A L P A G
97098 ACCGGCTACACGCTGCGGGCGTACCGCGGCACGGGAGTTGACCCGACCGACGTCGCCGAGCGGACACGAGACGCCGTTCTTGGCCCG
    >T G Y T L R A Y R P A R E L T P T D V A E R D Q D D P F L A R
97190 CCGGACGGCGTCCGAGACCGACGAGGACGAGGTTCATCTCGACGAGGAGGTGGCCGCCGAGTTCGCCGAGGCGGACGCGGAGG
    > R Q A V E T D E D E V I I L D E E V A A E F A E A D A E
97282 AGGCCGGCGGAAGTCCCGCTCCCGCAAGCCCCGCGCAGCGGACTCCGACGACGCGGAGCGCCACAGACGCGGACGCGGAGGAGGAG
    >E A G G K S R S R K P R A D A D S D D A G A A T D A D A E E E
97374 CCGGACTCCGACGAGGACGAGGCGGGCGACGAGGAGGTTCCGGTCTTCTCAGCCACCGGGGCGAGGTGCTGTGTTCAAGACGCCCGAATC
    >P D S D E D E A G D E E V P V F L S H R G R L L F K T P E S
97466 CCTCGTCAGCTTCGTCGGTCCGGCGCACCCACGACATGTCTCAACTGGACAGCTGGAATGAACTGTCCGAACGGGTGGAGCCGGCCGACA
    > L V S F V R S G A P N D M S Q L D S W N E L S E R V E P A D
97558 TCGTCCCGCTCGACGAGGACACCTACGAGCTGGACCTGGTCGTGGAGAACCTGCGGGGTGGGCACGACACCTGGGACTCGGCGTGTGATC
    >I V P L D E D T Y E L D L V V E N L R G G H D T W D S A L L I
97650 GAGCCGGCGAGGTGGCCCGGACGTCGCGTATGCCCTGCGTCTGCCCGCGGTGGACATGCTCTCCGCCGGCTCCAGCCTCGACGACCTG
    >E P A R W P G T S R M P C V C P C W T C S P A P A S T T W
97742 GACGAGGCGCTGCGCGCCACGGCCACGGCGGGCTCGGGGGCTTCTCGGGCGCGCGGGCTGAGGAAATCGGCGCGCAGACGGCGGAGTC
    > T R R C A P R P T A G S G A S A A G G .
97833 TCGGTTGGCGCACCATTTGTCGGCAAGATCTCTCGGGTCGTGGACTGGCGCGACTGACACGTTCCAGGGAGCATCAGTCTCTGGCAGAGAAAG

    BamHI
    junction marker

97925 ACCAGTCCCGGGAGGAGGACGCTGTGGCGCTCGTGCGCGTGTA CTGGGTCTGGCTCGGCGGATCCGGCCGACCGACCGGCCTCGGCC
98017 GGTTCGGCGCTGACGTCCGCTGTGGTCGACGACGAGTCCGGCTGCTCCATGCTCGGAGATCGGGCAGCAGCCAGCCGGCTACGCTCAGCT
98109 GGTCTGTCTACTCTGTGAGCGGTGCGGGCGGGCCGAGCGGGGTGCGATCGCCGCCGACAGCGCAGCACCACACGGTACCTCGCTGCTGAGTG

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FIG.11A(85)

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98201 CCGCCGGGCGTCCACTGGCGATCGCGGACGACGACTCGGTGGACGACTTCGCCGAGCGGTTGCCCGACGACGACTCGCTGGAGGAGATGCA
      > M Q
98292 GTCCGGCCGGCCGAGCGGGGCGGTCTGGGCTGGCCCGGGCGCTCCAGGCCGGGCGCTCTCGGGGTACCCCTCCCGGCGCCCGGGGATC
      > S A P A E R R A V G L A R A L Q A G A L S A V T L P A P R D
98384 TCGCCGGCTACAAGCAGGTCTCTCGGCGCAGCCGCGTCTGCCAGCGCCGGACTCCGCCGCCGTGGCGCTGCCGAGGTGCTGCGGGGAG
      > L A G Y K Q V L S A H A A L A S G R H S A A V A L R E V L R E
98476 CTCTACCCGGCCGCTGCGCGCGTACCCGGACCCGGCCGAGCGGTGCGCCTGGCCGTGTTGGACGCCCTGCCCGAGCCCGGGATGCTGGG
      > L Y P A A L R A Y P D P A E P V A L A V L D A L P E P G M L G
98568 CGGGACGATCGCCCGGGCCGGGAGGTGTCGGTGGCGGGGACGCCCATCGCCGCCACCTCGGGCCGACGGGGTGGCCGACGAAGGCAAGA
      > G T I A R G R E V S V A A D A I A H L A A D G V A D E G K
98660 TCAACGATGCGGTACCGCGTGGGGTGCCTATGCCGAGACCCCGCGCGGGGTCAGCCGGGCGTCACTCCGCCGTGGCGGAG
      > I N D A V T A L R V A I A E T P R A A V S R A L T S A V A E
98752 ACGGTCCGTAGGCGGTGGCTCGGTGCGAGCATGCGACGCGGTGCGAGGCCCTGGTGGCGCGCTCGACGCCCGGTCAACACCCCCAG
      > T V R Q A V A S V R A C D A G C E A L V G A L D A R V T T P T
98844 CCCGGTCCCGGGCGGGCGCCGCCGCGGGGCGAGCCGGTGCCTGCGCGAGTTGCCGGGCGCGGCTGCGCGCACTGCGGCCACACAGAGC
      > P V P G R R A A A R R G E P V A E L P G A G L R A L R P T E
98936 CCGAGCCGTTCCCGGCGCGGAGCCGTCCCGAGCCGGTCCCGGGCGGAGCCTGCCCGGCCAGCCCGCCCGCCGCTCGGCCCGCCCGGTC
      > P E P V P G R R S R P E P V P G G S L P A Q P R P L G P P V
99028 GCGCCGAGCCCGTCCCGCCGCGCGGTGCCCCGCGCCGATACCCCGGGCGCCTCGGGCCACCCCGCGGTCTCCGGCCCGCGCTCGCC
      > A P E P V A P P V A P R P I T P A A S A T P P V S G P P S P
99120 CGAGCCGCGCGCTGATCGACAACCCGGCCCAACCGCGCGGTCTCCGGCGCGCGCCCGCCCGCCACCGGGGATCACCCCGATCGCGCCGAGCC
      > E P R R L I D N P A N R P V S A P P P P P G I T P I A P S
99212 AGCGGAGCGGGTCCGTGCCCGCGCGGCGGTGAGCCGTTCCGGGCCACGCTGACCAACCGCGCGGATCCAGAACGCGGGCGGGAG
      > Q R E R G S V P P A E A G E P F R P T L T T A A I Q N A R A E

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FIG.11A(86)

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99304 CGGAGGCGACCATCATCCGGCTCGCCCCAAGACAGGGCGGAGTCCGCGCGCGCCACCGGGGGCTTCAGCGCCACCGACCTGAGCGT
>R Q R T I I P P R P K T T G E S A P P P T G G F S A T D L S V
99396 CCCGGTCCGACCCCGGTCCCGGCCAGGAGTCGCTCCCCGGCTCGCGGGCGAACTGGCGGTGTTCAACAACCCCGAGGACCCCGCGCG
>P V P T P R P G Q E S A P P G S R A N W P L V N N P E D P A
99488 ACAGTCCCGGAACAATCCGTCGCGCGGGGCCCTTGAGGATCGGGCGAAGCGGCAGATCGACGCGCCGACCCAGGTGTTCCCGCGCGGCC
>D S S P N N P V A R R P L E D R A K R Q I D A P T Q V V P P A
99580 GAGGGCGGGTCACCCCGCCTGGCTGCGCGACGACCTGCCCCAGGAGCCACCGATGCTGCGGGTGGTCGAGCCGCGCACCGCTGGCCGACCG
>E G R V T P P W L A D D L P Q R P P M L R L V E P P L A D R
99672 GGCAC TGGGATGGGCGGGCCAGGCTGCCGACCCGCGCTGGAGCCCGCGCTGCGGGTGGTCGACCGCGGCGAGGCAGCCCGCGCGG
>A L R D G P G Q A A D P R L E P P L R L V D R G E A A R A
99764 GCCGTCCGCGCGGAGCCCGCCCGAGCGGGCCCCCGGGAACACCGGTCCCGCTGGGTCAAGCGGTCCCGTTGGAGGAGCGGCCCGGAC
>G R P A P E P R P E R A P A E H R S P L G Q R V P L E E R P D
99856 ATGGAACATCGGACCGCCCCCGCAGCCGTGCGGTCCGCGCCGATGGAGGGCGTACCCCGCGCATCTCCGACGAGGGGACGGCGACCT
>M E H R T A P P Q P S R S A P M E R R T P P I S D E G D L
99948 GCTGATCTTCGCGCGCGCAAGTCGGCTGTTCTGCGGCACGGCAGCAGTCCGAGATGGACTGGTCGAGCACCGCCGACACCGGGTGGC
>L I F A A A K S A W F V G H G D E S E M D W S S T A S T G W
100040 AGGCGCGCGAGCGCGCGCGCGGTGGCGCGCGATACCAAGCGGGTTGCCCAAGCGGGTGCCGCGAGGCCAACCTGGTTCGGGC
>Q A A E Q A A R P A V G A D T K A G L P K R V P Q A N L V P G
100132 TCCCCCTCGCGGAGGAGTCCCCTACGGATAGTCCGCGACCGCGCGAGCCTCGCCGAGAAACACGACCGGCTACTTCGGGGGTGGCGTCG
>S P L R E E R P L R I V R D A A S L A E N T T G Y F R G W R R
100224 CGGGCAGGAGATCGCGGGTTTCGCGTCGGCGCGCGCGCGCGGCGGCGGTGGGACTTACCCGGGACACCGCGGACCGGAG
>G Q E I G G F A V G G R P G R E A A G G W D F T R D T G D R
100316 ACGACGACCGGGAGTACGAGTACCGGTCCGCGGGTACCGCTCCTGACCATCGCGCGGGGTGGCGGGCACCGCGCGCGCGCGCGCGG
>D D D R E Y E Y R S A G Y R S .
100407 CCGTGTGGCGTACGGCGGTAGCAACCGGACCGCCACCGGCGGTGGGACCACCGGAAGAGCAACCTGGCGCGCGCGCTGACGTC

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FIG.11A(87)

100499 CCGCAGGGACGGTGACGGCTACTGGCCGTCCCCCGGAAGGTTGCGAGGCGGTGCGGGGCGCACAGGGCGTGTAGGGCCGCTCCTGAGCCG
100591 CCCTACGGAATGGGCTAGCCCTACGGAATCGAGCGCCGCGCCCGGTGGCGTCGAGTTCCGCTCCAGCCGGTCCCCAACAGCCGGAC
100683 GCGCCGACGGCCCGCGGGTGCCGGTCGTGCGGGCGGTCCCGTCGTGATCAGGCCGGCGGACCGCGCGGCGAGCGCGGCATCGTGAGCA
< . A P A V A R S R R M T L V
100774 CGTACTCGACCAGCGAGATCAGCACGTGCTTCGTGACTCCCGGTTCCGGGCGTGCAGGCCACCCAGCGCACGTGTCGAGATCGCGAGC
< Y E V L S I L V H K T S E R N R A D C A V V P V D H S I A L
100866 GCGTCCCGGACGTCTGCGGGTCGTGGTACTGCATCCCGTCGAAGCAGTTGATGGCCACCAGGTACGGCAGCCGCCGATGCTCGAAGAAGTC
< A D R V D Q P D H Y Q M G D F C N I A V L Y P L R R H E F F D
100958 GATGGCCGCGAAGCAGTCGGCCAGCCGCGGGTGTGACCAGGACCACCGCGCGATGGCGCCCGGACCGAGCTCGTCCCACATGAACCAGA
< I A A F C D A L R R T D V L V V A G I A G R C L E D W M F W F
101050 ACCGGGTCTGGCCGGGGTGCCGAACAGGTACAGGATCAGGTCCCGGTGATCGAGATACGGCCGAAGTCCATCGCCACCGTGGTCGTCGTC
< R T Q G P T G F L Y L I L D R D I S I R G F D M A V T T T
101142 TCGCCCGGCACCTGCCGGGTGTCGTCAGCCCCACCGCGGGAGGTGATGCGCTCGGTGGTCAAGCGCGTGATCTCCGAGACCGAGCC
< E G P V Q R T D D V G V G A S T M I A E T T L P T I E S V S G
101234 GACCAGCGTCGCTTGCCGACGCCGAACCCACCGGCGATAACGATCTCGCCGACGTACCGCGCCCGCTCGGGACAGCGGGCGGTGCGGACA
< V L T T K G V G F G A I V I K A S T V R G S P V P R H S M
101326 TGTCAGAGCCTGCGAAGTCCACTCAGCACCCCTCTCCAGCAGTTCAGTGCCCAACCGGTCGTCGGAGTCGTCAGGATGGTCGGCTCGTGGA
< < . L R R L G S L V R E L L E T G V A D D S D D L I T P E H V
101417 CTGCGACCAAGCCGTCGGTCGCCATGTGGCGATGAGCACCCCTAGCCACGCGAGCGGGAGCTGCATCCGCGCCGCGATCTCGGCAAGCGAC
< A V L G D T A M D A I L V R A V G L P L Q M R A A I E A L S
101509 TGCACGCGTCGTCGCACAGCGGGCGATGTACTGGTCTCTGGGCCCTGGCCACCGTTGCTACTGGCAGCGGCCGACCGCGCACCGTCGT
< Q V R G D C L A A I Y Q H E R G Q G G N S S A A A R G R V T T
101601 CTCGACGAGCGCCTCCAACGCGATGTCCAGCCGAGGGCGGGTACGACCGCGGGTGACGGCGGTACGGACGGACCAACGCGCCAGTCGGCTCGT
< E V L A E L A I D L R P R T R G R T V A Y P R V L A G T P E D

FIG.11A(88)

101693 CACGATCCATGTGCGCGCTCACCTCTTGTCTCCCGACACCGGCTGAACCCGGTGGAAACCCGTCGTTCTTGTCTTGCACCCCGCCCGAC
< R D M D G S V E K T G S V
101784 CCATCGGCCAGCGGTGGTACAGCCCATCATCCACAGTCGTACGGGCTGCGGGGTCAACGGCTGCCCCACCCGGTCGACCGAGGGGC
< • G M M G V T T R P Q P T L A D G V R D V L L A
101875 CATCTCGTATCCGACCTGCCCGACGTGCGAGCTACGGCGGCGAGCACGGCGAAGGACGAGCGTCCGAGATGGACATCAGGAACAGGAAGC
< M E Y G V Q G V D C S R A A L V A F S S G D S I S M L F L F G
101967 CGTTGTCCATCTCGACCACGGTCTGCAGCACCGACCGCCCTCGAAGCAGCGTGCCTGCTCCCTGCGTGAGGCTGACCGCCGCGGACGCGGATC
< N D M E V V T Q L V A G G E F C R A A G Q T L S V L G S A I
102059 GCGGCGAGCTGGTCGGCCCGGTACGCGGAAGGTCTCGTGACGACGCCAGGAGCAGACCGTCCGCGGAGACGGCGACCGCGTGC GCGACACC
< A A L Q D A R D R P L D R S S A L L L G D A S V A V A H A V G
102151 GGGCACCCCGTCGGCGAAGTTGGCCAGCAGCAACCGAGATCCTGCGTAGTTGTATCCTTGTGCTCCTTCTGCCCGCTCCCGGCCACCG
< P V < • G Q Q E K Q G S G A V P
102242 GGCCTGAGCCAGACTGCGAGGATTGCTGCCACCCGAGCTGCCTCCGGGTTGGTCGGGTTGCCGTGGGCTCGGTACGCCACGCTGCACG
< G S G S Q S Q Q G G P A A E P N T P N G D P E T R G R Q V
102334 CCTCGATGGTATGCCGAGAGCAGACCGCGGACGCCCTCCGGCTACGGCGTGGACCGACGTGGTGGGCTTCTCCACCCCGCCAGGCACGAG
< G R H Y A S L L G R V G E P T R R Q V S T T P K E V G G P V L
102426 TTGGGCCCATCGGCACCCGCTTCGGCAGGCCCTTCGGGTGGTCTCGGCCACCGGGACCTCGGTGGCCCGCGAGGCGGCCCGCCAGCCGTCGT
< Q A M P V R K P L G K R T T E A V P V E T A A S A A R W S P P
102518 CCGCGGCAGTCTGCCAGGCGTGGGCTGCGGCGTGGGCCCGCGCGGCGAAGCCCTCGGCGGGACCGGGGCGGTGCCACCGTTGTTCCGGC
< A A T Q W A H A Q P T P R R G A F G E A P G P R T G G N T P
102610 GACCCGTTGTGCGCGGCACTCTCCGGCCATCGGGGTGTCTGCCATCGGTGCGTTACCTGCTCCTCCGGGTGCTGGTGTCTGGACGGGCGG
< S G N D R P M G G A M P R D A M P A N G T T G P A P T Q V P R
102702 GCCGGTGACGTGACCGCGGAGAACTGTTGGGTACGGCGGCGTTCCGGCGGCTCCCGCGGCCATTGGTCGCGCGTGGGCGACGCCGGCGG
< G T V D V A S F Q Q T V A A N A P S G A G N T A R Q A V G A T

FIG.11A(89)

102794 TCTCTCCGAACCCGAGCGGGGTACGGAACAGCCGACTCGAGTCCCGGAAGATCGGCAGCTCCATGTCGTCTCGTCGCGTACCGCTGC
< E E S G S R R T R G W A S E L E R G I P L E M T E D A Y R Q
102886 TGCCGGTTCTGGGCTGCACGGGCGTCGACCGCGCGGTGGCGGGGTGCTCGGCTGGTGGCGGCGTGCTCGGCACCTCGGTGCTCGG
< Q R N Q A Q V P T S R A P T P T P Q T A P T S P V E T S P
102978 CACCCGGGCGAGTCCGTGGTTCATGTCCAGGGCTGCGGCGAGGCGCTCCGGCACCGCGGGGTGACCGGCTCCGGCGCGGCCACCGCGGGC
< V R P L E T T M D L A A A L R E P V P P T V P E P A A V P P W
103070 AGGCGGGCGGCCACGGGCGCTGGGCCGACGGGACCGGCCGACTGGGCAGCGGCTGCGCGAGTACGGCTGACCGGACACGGGCGTGCCG
< A P P A V P A Q A D P V P R S P L P Q A S Y P Q G S V P T G
103162 AACGGTGACCGGAGACGGGCGTGCCGAACGGCTGACCGGACACCGGGCGCGAGACGGGCTGACCCGAGACCGGGAAGACGGAACCGG
< F P Q G S V P T G F P Q G S V P A A S V P Q G S V P F V S V P
103254 CGGTGCGGACACCGCGGCACCGAGACCGGTGGCGGGTCCAGCCCGGCTCGGGGTGCTCGGCAGCTGTCGGGGATGGCCGGCTGCT
< P A S V P P V S V P P T W G R A E P S S P L Q R P I A P Q Q
103346 GGCCGCTGTCGCCGGATCGCCGTGCGCGACGCCCGCGCTGCGGACGGGTGCTCGACTGGCCATTGAGGTGCGGCGCGCGCGGCA
< G S S A P D G D G S A R R Q P L P D S S Q G N S T R G A A
103438 CCGCCAGCGTGCCACTGGCCCCGTGAGTCCGACAGCCGCGCATCGACCGCATGGAACCGTTCGACCGGGCGTGCCGTGGCCGTTGCG
< G G A T G S A G T L D S W A P M S R M S G T S A P T G H G N R
103530 CGAGGCCGGTTCGAACGACCGCGCCAGGGTTACCTGGTTGCCGAGTGCCCGCGCGTGGGTGGCGCGCGGTGTCGCCGGGTTGTTGC
< S A P D G D R G G L T V Q N G S H G P R Q T P A P T A P N N G
103622 CGAAGCCCGAAGGCACCCAGGGCGGGGGCCCCCGGCTGCGAGCTGGTGAGCGAGGCGGGAGGGCGCGCAGCGCGCGGGCTGC
< F A A F A G L A P P A G G P Q S S T L S A P P A P L A G P Q
103714 TGAACCGCGGAGAGCGCCGGGCACCGACGCTGGTGGGAGGTGACGTGCGCGACGCTCCCGCGTGGTGCCGGCGCGCAGCTC
< Q F R G S L A R P V L V T T P L T V D A V T G R D T G P R L E
103806 GACCTTGACCCCGTCCGGGACGCCAACCGGGCGACCAACAGGCCCATCATCCGGGAGACGGCCACGTCCACCTGCGGCGCGGAGCGGA
< V K V G H R S A L R A V V V L G M M R S V A V D V Q P P S A L

FIG.11A(90)

103898 GCGGTCGTGAGTCTGTCGGCGCTGATGCCGATCCCCGGTCTCGACGTAGAGTTGGCCCCGGTCGCCGACCCGGCGGGCC
< R D N L D H L Q E A S I G I G R D E V Y L N A R D G V R R A
103990 TCCACCATCACCTGCGAGTCGGCGCGGAGAGCGGTGCGTTGTGGAACAGCTCGGCGACCAAGGTGGACCAAGTCTGTTGACCGCGTGC GC
< E V M V Q S D P P S F A T A N D G L E A V L H V L D N V A H A
104082 GCGACCTCGATGTCACGGTCGATACCCCGAACTCGATCCGGGTGTAGTCTCGACCTCGGACTGGCGGCGCCGCGACGTCGATCAGTG
< A V E I D R D I V G F E I R T Y H E V E S Q A A R L V D I L A
104174 CCGCGGCTCGCGTGCACGCGGTGGAGTCGGCCCCGGCGAGCACAGAGTTCTCGTCTGCGGCGCATCCGGGTGGCCAGGTGGTGC
< A P E R Q V R T S D A G A L V L L N E D N R R M R T A L H D
104266 AGCTGGAACAGCTCGGCCAGCCGGTCCGGTCTCTCTGCGCGCTCCAGCCGGTCGAGGTGGCCGATCAGCCGGTCGACCAAGGATCTGCGA
< L Q F L E A L R D P D E E G R E L R D L H F I L R D V L I Q S
104358 ACGCGGGCCAGGTTGACGAACATGGTCGCGACGGAGGCGCGCGCTGCTCGCGCGCTCCGTACGGCTCCAGGTGGACCGCGT
< R R A L N V F M T A V S A R L A A Q E A A T R V A E L H V A N
104450 TGAACGCCTCGGTACCTGGCCGAACCTGCTTGTGCGCACCGGCGGTCGGCGATCTGTTGGCCGCTGCACCGGGAGAGCTGG
< F A E T V Q G F E D K S R V P L P E A I Q N A A Q V P S L Q
104542 CTGGAAACTCGCGATCGCGCAGCGCGCAACGGCCTGGGGCAACCGTACTGGGCGATGCTGAGCGCACCCCTGGCGCAGGTGCGCAGCGA
< S S G Q P D R L R A V A Q P L G T Q A I S L A G Q R L D R L S
104634 GCGGGCCATCGACCGGGCGACCAAGTACGCGAACAGGATGGCCAGCAGCATGCCGAGCAGCAGGCGGCTCTGGAGGAACACCGTGCCT
< R A M S R A V L Y A F L I A L L L M G L L L G T Q L F V T R Q
104726 GTACGTCGGAGCGGCGTGGCCTGCTTGACCACGTTGCCGTCGAGCTTCGCCCTCGACCGTACGGATCAGTTTGGCGCTGGCGACCATG
< V D S R L A D A Q K V V N G D L K A E V T R I L K A S A V M
104818 GCCGCTCCACTGATCCGGCCCGAAGCGCGCTTGCCCATGCTGCCGTTGGTGTGGCTCGAGCCAGCCGGTGTAGTTCTGCGCCTCGCG
< A A D W Q D P G F P A N A M S G N T N G D L W G T Y N Q A E R
104910 CCGGTCGCGCGCGGACGGTCTGGTCGTGAGGTCCGACTCGTCCAGGCTGGCCACCGCCTTGAAGCTTTCAGTGCCTGCTGTCGCGCGG
< R D G G A V T Q D H L D S E D L S A V A K F S Q L A Q Q Q G T

FIG.11A(91)

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105002 TGCCGCTGGCGATGTAGTCGGTGGCAGGATGGGGTCAACTCGCGCTGGATCAGCGCCGGTGCACCAACCCGGCGGACCGAGAGGTAT
      < G S A I T D T R L I P T L E R Q I L A R H V V V R R V S L Y
105094 TCCTTCTCCGGGCGACGGCTGCCGGGCCCGCATCCGGTCGTCAGGTGTTGTACCCGGCGAGGTGGTGGCGGAGTCGCGGATGGACAG
      <E K E R A V A A A A R M R D S L D N D G A L H T A S D R I S L
105186 CAGTTCGTTGATCAGGCCCTCGTACGCCTGCATGGCGTCGATGATCTTCAACTTGCCGTTGAAGACCTGGCTGCGGGTGCCGGGAGGTCTCT
      <L D N I L G E T A Q M A D I I K L K G N F V Q S R T G P L D K
105278 TCAGGTTCTGGTCGATCCCGTCGAGGAGGCCCTCCAGGCTGCTCGGCAGGCCGTGCACCTCCCCCGCTGTTGCAGGTACGGCACCTTGTC
      < L N Q D I G D L L G E L S S P L G D V E G R Q Q L Y P V K D
105370 TGGTCGACCCGGATGTTGACCCGGTTGTACGCCTCCTGGTACTGCGCCTTGGCCTGGTCGCGCTCGCCCCGAGCAGCAACACCGCGGAGGT
      <Q D V R I N V R N Y A E Q Y Q A K A Q D G S A G L L L V A S T
105462 GCGTTCGTCCTGGAGGCTGTTGACCAAGTCGCCGAGTAGCCACAGATTGGCCAGGTGCGCGAGCGGTTGGCGTTGTTACGCGTTTCCA
      <R E D Q L S N V L D G S Y G V L N A L D G S R N A N N L T E L
105554 GGTTGTCGACGAGGCCACTGGTGCCGACGACCGTGGCGATGGTCGGCAGCATGATGAGACCGAGCTTGGACCAGATCGGCATGTC
      < N D V L G S T G V V V T A I T P V I M I L G L K S E I P M
105645 GCGGAGCCGGCCGACCGCCGACGCGAGTCGCGACAGGAAGAACCCCGCTTCGGTCTTGCTCAGTCAACCGCCCTCGCGATCACAGC
105737 GTTCGCGCGTTGCCCGGGCAACGCTCAGCGACCGACCCGGCGGTGCGACCTCCGAGATTCCATCAGCCGTGTTCCAAAGAGAAAGCCCA
105829 GGCTGGCCGTCGCCGAGGTGTGATGAGATGTTGATGCAATTTGCTCGCAATCCGTCCAGCCGGAGTGACTGACAGTAATGGATCACCCC
      > M D H P
105919 CACCGCCTCGTCTGCTCGCCGGCCCTTCGGGCTCCGGAAGTCGTACATAGCCCAACAACCGGGCTTCCTGTCTTTGTCTGGACGACTT
      > H R L V L L A G P S G S G K S T I A Q Q T G L P V L C L D D F
106011 CTACAAGGATGTTGATGACCTACGTTACCGCGCCAAACGGTCTTGTGGACTGGGACTCACCCCACTGCTGGGACCGCGGGCGCGGTGG
      > Y K D G D D P T L P R Q N G L V D W D S P Q S W D A G A A V
106103 AAACGATTGCCCGGCTGGCGGGGACGGCAAGGCCGAGTGCCTGTTATGCGATCGGCGCGGACCGCGGGTGGCCACCGGACATTCGAG
      >E T I A R L A R D G K A E V P V Y A I G A D R R V A T R T F E

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FIG.11A(92)

106195 GTCGCCGATCGCCACTTTTCGTCGCCGAAGGATTTTCGCCGCCGAGATCGTCAGGAATGCCAGCGCGAGGGCTGCTGCCGGGGCGTA
> V A G S P L F V A E G I F A A E I V E E C R R R G L L A G A Y
106287 CGCGCTGCCGCCGCCGCGGCACCACTTTTTCGGCGGGCTGCCCGACCTGGCCGAGCAGCGCAAGGCTCCCGGGATGCTGCTGCGGC
> A L R R P R G T T F F R R L A R D L A E Q R K A P G M L L R
106379 GCGGCTGGCCCTGCTGCGCGCGGAGCGGGGTGCTGCGCCGCCAGCGGGGGCTCGGGCTCACCCGGCCCGCGCGAGGTGCTGCGC
> R G L A L L R A E P A V L R R Q A G L G A H P A P A R E V L P
106471 CGGGTGGCCGACCTGCTGCCGGGCCACCCGACACCCCTGATCAGCCAGCAGCTTCCCGTACGCCGGCTTGATCACCTCGTCGATGAT
> R V A D L L A G H P H H P • • G L L K G Y A P K I V E D I I
106561 GGCCAGCCGCTCGTCGAACGGGATGAACGCGCTCTTCATCGCGTTGATGGTGAACCATTTGGAGCTCCTTCCAGCCGTAGCCGAAGGCCTCCG
< A L R E D F P I F A S K M A N I T F W Q L E K W G Y G F A E A
106653 CCAGCAGCGCCATCTCCCGGACATCGAGGTGCCGCTCATCAGCGGTTGTCGGTGTTCACCGTCAACCCGGAACCGCAGATCGCGCAGAAGC
< L L A M E R S M S T G S M L R N D T N V T V R F R L D R L L

BamHI
junction marker
106745 CCGATCGGGTGTCTCGCGGATCGACGCCGCCGCCGGTCTGCACGTTCCAGCACGGGCACAGCTCCAGCGGGATCCGCTTGTCGCCGACGTA
< G I P H E A I S A A A G T Q V N S S P C L E L P I R K D R V Y
106837 CGCGGCCAGCGGCCCGGCGGTGCGCGGGGGTGATGTCTCCACGATGCCACCCCGTGCGCGAGCGGTCCGCGCCGACCACT
< A A L R G L V P P D G P T I D D V I R V G H G L R D A G C W Q
106929 GGATGGCCTGCCAGATCGACGGCAGCCCGAACGCCCTCGCGGGGTGAATGGTGAAGTGAAGTTCTCCCGCTGCAGGTACTCGAAGGGCTCC
< I A Q W I S P L G F A E G A H I T F H F N E R Q L Y E F A D
107021 AGTGCCGGTGGCGGGAATCCCGCCTCCGCCCGCGGATGTCGAAGCCCAACCGCGCGGTGCGGTGCCGACCGCCAGTTCGGCGAT
< L H R T P P F G A E A G A I D F G V V G A D R H R V A L E A I
107113 CTCCTGCACCGGGCGGTGCCGCATGGCGGTGAGCAGGGTGCCGACCCGGATCGGATGGCGGGGTGCGGGCGGAGCGCGGCCCTCGG
< E Q S R A A H R M A T L L T G V R I P H G A D A A L A G E A

FIG.11A(93)

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107205 CGAACCCGGGACGACCGCCTCGACCACCTCGTCCAGGGTCAGGTCCCGCTCCAGGTGCTGCTCGGGGGGAACCGCACCTCGGGCGTAGACG
    < F G A V V A E V V E D L T L D R E L H Q E P A F R V E A Y V
107297 ACCCCGTGGGGCCAGGTCCAGCGCGCACTCCTGGGCCACCCGCCGAGTGGGGCGGGTCTGCATGACCGCCACGGTGTGGGGGAACGT
    > V G D A A L D L A C E Q A V R R L A P A T Q M V A V T H A F T
107389 CTCAGGTAGCGTCCAGCGAGCCGGAGTTCGCCGCCGACGAACAGCGGCCGAGCGCTTCCGGGTGGTGGGACCTTGAGCATGTCCTCG
    < E L Y R E L S G S N A A A V F W R G L A E P D T T P L E H G V
107481 CCTGGGGGCCAGCTCGACGATCGTCGGCGGCCGAGGCCGCGTCGAGGTCTGCAGCAGCAGCGCCTTGGGGACCTTGAGCATGTCCTCG
    < E A A L E V I T A P R L G G D L H D H L L A K P V K V I D E
107573 TATGAGATTGCGACCATGCCAGACCCTAGTAGCAGCCGGGTGCGCCGACGCGACCGGCTGGGAGGATGTCCAGGTGATGGACCCC
    < Y S I A V M          > M D P
107662 CGCATCGTCGACCGGCTGCGTTGCCCGGTCTGCGCGGAACCGCTCACGAGCGCGCGCGGGACACCCGGGGCGCTGCGCTGCCCGCGCG
    > R I V D R L R C P V C A E P L T E A A A G T T R A L R C P R R
107754 GCACAGCTTCGACGTGGCCCGCCAGGGGTACGTGACCTGCTCGCCGGCGGGCCCCCGCACGTGGCGGACACCGCCGAGATGGTGGCGGCC
    > H S F D V A R Q G Y V D L L A G R A P H V G D T A E M V A A
107846 GCGCCGACTTCCTCGCCGCGGGCACTACGACACGCTCTGGCCGCGCTCGCCGCGCGCGCGCTGAGCCACCCGCGGAGGCC
    > R A D F L A A G H Y D T L S A A L A A A L A L S H P P E A
107938 CCCGGAGGGACGCGTCGGCCGGCAAGACGGGAGGATGCCCAAGCCGGCGGGGATGCGTCCGCTGGACATGACGCGTCCGCCGGACAGCC
    > P G A D A S A G K D G Q D A Q A G R D A S A G H D A S A G Q P
108030 GGCCGTCGGGACGTACCCGCTGGTGGACCGCGGGGGGGGACGGGCCGGCACCTCGCCGCGGTGCTGGCGGCGCTGCCCGACGCGCGTGG
    > A V G T Y P L V V D A G A G T G R H L A A V L A A L P D A V
108122 GCCTGGCCCTGGACGTCTCAAGCCGGCGCTGCGCCGGGCGAGCGCGGGCCCCACCCGCGCGGGCGGCGCTGCCGACACCTGGCGGGCGG
    > G L A L D V S K P A L R R A A R A H P R A A A L A D T W R R
108214 CTTCCGCTGGCCGACGCGCTGCCGTGCTCGACGTCTTCGCCCGCGGCAACGGCGGGGAGTTCGCCGGGTGCTCCACCCGGCGCG
    > L P L A D A S V A V L L D V F A P R N G A E F R R V L H P A G

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FIG.11A(94)

108306 CGCGTGTCTGTGGTCACCCCGCGAGGA CACCTCGCCGAACGTGTCGACTCGCTCGACCTGCTGAAGGTGACCCCGACAAAGGCGGACC
> A L L V V T P A E D H L A E L V D S L D L L K V D P D K A D
108398 GGTGCGCGGAGCCTGGCCGGCCACTTCGAGCAGACCGCGAGAGCGTGTGCGGGCCCGGCTGGAACCTACCGGCCGCGCAGGTGGCCACC
>R V A G S L A G H F E Q T A E S V L R A R L E L T G R Q V A T
108490 CTGGTCGGGATGGGACCCAGCGCTGGCACACGACCGGCCACCTCGCGGCCGGATCGCCGCGCTACCCGAGCCGGTCCGGGTGACCT
>L V G M G P S A W H T D P A T L A A R I A A L P E P V R V T L
108582 CGCGGTACGGCTCGGCGTGTACCGCCCCGCTGACCGGGCGGCGCGCTCAGGTGGAAGTGCACCTCTCCAGCCCCGGCGGCTC
> A V R L G V Y R P R • < • T S L D V E E W G P P E
108674 CTCGTGTAGGGCCCTCGCAGGACCACGCCCCACTCCAGGCCACCGGCGCTGCCGATCGCGTTGGCTCGACCAAGGCCGGCGGCGGACC
< E H Y P G R L V V A W E L A W R R Q G I A N A D V L G P P S R
108766 GCCCGTCGCGCTCCAGTCCAGGTACGCCCAGTCGAGGCGAGTAGTGCAGGTGCAGCAGGCCCGCGCTGCGCCGGGTGCTGGGCGCGGCG
< G D R E L E L Y A W D L C Y H L D L L A A A D A P H Q P A A
108858 AGGATCGGGAGCGCCACTGCTGGAAGCTCTCCCCGCCGCGATGTGCGGCAGCCGCTCCACCAGCCGCTGTCGACCGGCAGCGTCGGGTC
<L I R S R W Q Q F S E G G A I H P L R E V L R E D V P L T P D
108950 GAGTGTCTGGCCAGGCCGAGCACCCAGGCCAGGAGAACAGCGCGTGTGTGCAGCACGAACCGGTGGTCGCCCCGCGCCCATCA
<L Q K A L G L V W A L S F L A D H H L V F S R H D G R G M V
109042 CGAAGTCCACTCCGGCGGGGTGACCAGGTGACCAAGTGGGAGTTGAGCAGCCAGCTCATCGCCGCTGCGCCGGCATGCCGAAACACCGG
< F Q W E P P T V L D V L H S N L L W S M A A Q A P M G F C R
109134 GCCAGGATCACGTGCAGCAGCGCGATGCGCGCTCGATCTCGACGGTCGGCCGCGAGCTCGATCTGTCGCCCGGCTCCACACAGGGGAA
<A L I V H L V A I R A E I E V T P R L E I E D G P E W V
109225 ACTGGTCGGTGGCAGCGGCCAGCCAGCGGACAGCTCGTCCAGGTGGCGTACGGACCTCTCGGGGTGGGAGCGGAAACGCGCACG
109317 GCTCAGATCCCTGTAGTCGCATCGGCTCAGTGCCGGTCTGCCCCCTTGGCTGGGAGGATAGCGGTTACGACGAGCGGCACACGGCGGG
109409 CGGGGGCGGGCGGTTACCGCATCCGCTCGATGACCAGCGGCTGCGGGGTGCGGGCGGTGCGGCGAGATCCGTACCGCCCGGACCGGCTCG
BamHI
109501 GCCAGCGCGCGGGGATCC

FIG.11A(95)

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1  GTCTTCGGGGAAACCCACGGGAACCTCCTCGGCAGAACCGGACGAGCTGACCGTAAACGGTGGGACCCGCGCGGATCAACCGGTGGTGGTTCCTCCAGGTTCCGGCCGCGCGGCCCGG
122  ACGCACCGCCCGCGGTGTGAGAAAGGGACCCATCTCTACCGTAGCGGTTAACAAAGGGGCCCTTCCTT TCA CCG CAG GTG CAG GAC GTC TCC TGC GGC GAG GGT GCG
      < * R L H L V D G A A L T R
228  CGG GCC CGC GGT GTC GAC CAG CAG CCG GGC GTC CAC GCC GGT CGC CAC GGC GUT CAC CTC CGC ACC GCC GGC CAG CAG CAC
      < P G A R T D V L L R G D A D V G T A V G T V E A G G P L L V
318  CGG CAC CGG TCT GCC GAC CGT CGC GCA GGC CGC CAG GTA CGC GTC GCG CAG CCC GGT GGC CAC CGC GTC GCC GGC GGC GTG GCG CCA GCG
      < R V P R G V T A C A A L Y A D R L G S A V A D G G A H R W R
408  GTC GTA CCA GTC GGC GAC AGA GCG CAG CAG TGC GCG CAG CAG GTC CCG GTC GGT GGC GAC CCC GGC GAG CTG GAG CGA GGT GGC
      < D Y W D A V S R L L A R L L P D R D T A V A G A L Q L S T A
498  CGG CAG GCC GGT CGG GTT CGC CGG CAG CTC GTC GGC GCG CAG GGT GAC GTT GAG ACC GAT GCC GAG GAC GAT CGC CGG GGC CTG GTC CGG
      < P L G T P N A P L E D A R L T V N L G I G L V I A P P Q D P
588  GGC CGG GCC GGG CAC CGC CTC GGC CAG GAT GCC CGC GCA CTT GGC GTC GAT CAG CAG GTC GTT GGG CCA CTT GAG GGC GGC GTC CAG
      < A P G P V A E A L I G A C K A D G I L L D N P W K L A A D L
678  CTC GGC CAG CCG GGC CAC CGC CTC GAC CAG CGC GAC GCC GGC CAG GCG GAG CAG CCA GCC GTA CCC GGT CGC GGC GGC CGG CCA GTC
      < E A L R A V A E V L A V G A L L P L W G Y G T A P A P W D
768  GCG CTC CGC GAC AGC CTC GCC CGG CGG CAG CAG GCT GGT CGC GAT TCC GGC GCG GGG CGG CGA CTG CCA GAC CCG GCC CGG CGG GCC
      < R E A V A E G P R L L V S T A I G A R P S Q W V R G R G
858  CGG GCC GGC GGT CTG CCG CTC GGC GAT CAC CAG GAG GCC CTC CGG CTC GGC GGC TCG GGC CGC CTC CGC CAC GTC GTC GGT CGA GCC
      < R G A T Q R E A I V V L G E P E G S R A A E A V D A N T S G
948  GGT CTC GGC GCG TAG CTC CAG CCG GGC CCA GGC GCG GGT GAG CCG CGG CAG CCG GGC CGC CGA CAG CGG GCG GCG ATC
      < T E A R U E L R A W P G H P A T L A R R L R A A S L P P R D
1038  CAG GTC GGT GTA CCG GCA GCC GGC CAT CCCGCCAGCCTACGGCCCGCCCGGACGCGCGCGGTGCGCGGCTTCGCCAGCCCGGTGAGGTGCTGA GGC GTA CTG
      < L D T Y P S G P M
1145  CAC ACC GTC GGC CAC CTG AAC CAT CGT TAT ATT CCG TGG GTG ACT ACC GAG ACC GGG ATC AAC ATC CAC AGC AGG GCG GGC AAG CTG GCG
      > V T T E T G I N I H S T A G K L A

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FIG.12A

1235 GAC CTG GAG CGA CGG GTC GAC GAG GCG GTG CAC GCC GGA TCG GCG CGT GCG GTG TCC AAG CAG CAC GCC CGG GGC AAG AAG ACG GCG CGG
 >D L E R R V D E A V H A G S A R A V S K Q H A R G K T A R
 1325 GAG CGG ATC GGG CTG CTG GAC GAG GGG TCC TTC GTC GAG CTG GAC GGG TTC GCG CGG CAC CGG TCC ACC AAC TTC GGC CTG GAC CGC
 >E R I G L L L D E G S F V E L D G F A R H R S T N F G L D R
 1415 ACC CGC CCG TAC GGC GAC GGG GTG ATC ACC GGC TAC GGC ACG GTC GAC GGG CGG CAG GTC TGC G'rC TTC GCG CAG GAC TTC ACG GTC TTC
 >T R P Y G D G V I T G Y G T V D G R Q V C V F A Q D E T V F
 1505 GGC GGC TCC CTC GGC GAG GTG TTC GGC GAA AAG ATC GTC AAG GTG ATG GAC CTG GCG ATG AAG ATC GGC TGC CCG GTC GTC GGC ATC AAC
 >G G S L G E V F G E K I V K V M D L A M K I G C P V V G I N
 1595 GAC TCC GGC GGC CGC ATC CAG GAG GGC GTG GCG TCC CTC GCG CTC TAC GGC GAG ATC TTC CCG AAC GTC GCG GGC AGC GGC GTC
 >D S G G A R I Q E G V A S L G L Y G E I F F R N V R A S G V
 1685 ATC CCG CAG ATC TCC CTG ATC ATG GGC CCG TGC GCG GGC GCG GTC TAT TCT CCG GCG GTC ACC GAC TTC ACC GTG ATG GTC GAC CAG
 >I P Q I S L I M G P C A G G A V Y S P A V T D F T V M V D Q
 1775 ACC TCG CAC ATG TTC ATC ACC GGC CCC GAC GTG ATC AAG ACG GTC ACC GGC GAG GAC GTC GGG ATG GAG GAA CTG GGC GGT GCC CGC ACC
 >T S H M F I T G P D V I K T V T G E D V G M E E L G G A R T
 1865 CAC AAC GCG CGC AGC GGC AAC GCG CAC TAC CTC GGC ACC GAC GAG GAC GCG ATC GAG TAC GTC AAG GCG CTG CTG TCG TAC CTG CCG
 >H N A R S G N A H Y L G T D E E D A I E Y V K A L L S Y L P
 1955 TCG AAC AAC CTG GAC GAG CCG CCG GTC TTC GAC GCC CCG GCG ATC AGC GAC GCC GAG CTG GAC AGC CTC GTC CCG
 >S N N L D E P P V F D A P A D V A I S D A D R E L D S L V P
 2045 GAC TCG GCG AAC CAG CCG TAC GAC ATG CAC CCG GTC ATC GAG CAC GTG CTG GAC GGG GAG TTC CTG GAG GTC CAG CCG CTG TAC GCG
 >D S A N Q P Y D M H R V I E H V L D D G E F L E V Q P L Y A
 2135 CAG AAC ATG GTG GTC GGC TTC GGT CGA ATC GAG GGA CGA CCG GTC GGC GTG GTC GGC AAC CAG CCG ATG CAC CTC GCC GGC ACG CTG GAC
 >Q N M V V G F G R I E G R P V G V A N Q P M H L A G T L D
 2225 ATC GCC CCG TCG GAG AAG GCC CCG TTC GTG CGC ACC TGC GAC GCG TTC AAC ATC CCC GTG CTG ACC TTC GTG GAC GTG CCC GGG TTC
 >I A A S E K A A R F V R T C D A F N I P V L T F V D V P G F

FIG.12B

2315 CTA CCC GGC ACC GGC CAG GAG TGG GAC GGC ATC ATC CGG CGC GGC GGC AAG CTC ATC TAC GCG TAC GCC GAG GCG ACC GTC CCG AAG GTC
 >L P G T G Q E W D G I I R R G A K L I Y A Y A E A T V P K V
 2405 ACC GTG ATC ACC CGC AAG GCG TAC GGC GGC TAC GAC GTG ATG GGC TCC AAG CAC CTG GCG GCG GAT CTG AAC TTC GGC TGG CCG ACC
 >T V I T R K A Y G G A Y D V M G S K H L G A D L N F A W P T
 2495 GCG CAG ATC GCG GTG ATG GGC GCG CAG GGC GTG AAC ATC CTG TAC CGG CAG GAG CTG GCC GCG GCG GAG GAC CCG GCG GCC GTG CCG
 >A Q I A V M G A Q G A Q G A V N I L Y R Q E L A A A E D P A A V R
 2585 GCC GAG AAG ATC GCC GAG TAC GAG GAC ACC CTG GCC AAC CCG TAC GTC GCC GCG GCG TAC GTC GAC TCG GTG ATC CCG CCG CAC
 >A E K I A E Y E D T L A N P Y V A A E R G Y V D S V I P P H
 2675 GAG ACG CGT ACC CAG ATC GTC CCG GCG TTG CCG GTG CTG CCG ACC AAG CCG GAG ACG CTC CCG GCG AAG AAG CAC GGC AAC ATC CCG CTC
 >E T R T Q I V R A L R V L R T K R E T L P A K K H G N I P L
 2765 TAG GCCTGTGAGGGGCCCTGTACGGATCGTGCAGAGGGGCCCTCCGACGGCGAGAGCGCGGGGCCCGGAGCGCGGCGCGG TCA GCA CCG CCG GTT
 > • < • C A P N
 2878 GGC GGC GAG GCA CAT CCG CCG GGC GGC CGT GCG GCC CAG TTC GAG CAG CTC CCG GTC GCT GGT CTC GCG GGC GGC GTC CCG CCC GTC GAC
 <A A L C M R A A T R G L E L E A D S T E R P G D P G D V
 2968 GCC CAA CCC GCG CTC GGC CAC GAT GAC GGT GAC CAG GTC GCC GAC CCG GAC GAT CAT CCG GGT TTC CCG CCG GTA CCC CAC GTC GAG GGG
 <G L G R E P V I V T V L D G V R V I M R T E P P Y G V D L P
 3058 CTT GCC CGT GGT GGC GTC CAC CCG GGA CAT CAC GGT GTG CCG CAA CAC GAC CCG CTC GTC GCC GGC GAA GTC GCG GGC GAT CGT CTG CCA
 <K G T T P D V P S M V T H R L V V A E D G A F D R A I T Q W
 3148 GGT GTG GGC CAC CGA GAT CCG GCC GCG ACC GCG GGC CCG AAC CCG CGT GTC GCT CCA GCG GGC GCA GGT GGT CCG CCG CCG GTC
 <T H A V S I A G R G D D L P R V A T D S W R A C T T A A R D
 3238 CAG GTC GGC GAG CAG CCG GCC GGC GGC GTG GAG GCG GTA GAC GTC GGT GAG GAC GGC GAC GGC CAT CGA CCC GTC CTG GGC
 <L D A L L R G A P A P D L R Y V D Q T L V P V A M S G D Q G
 3328 CGA CGT GTC CAG GAG CAG CGT CTG GGA TCG CGA GTA GCG AGA CAC CCG CCG CCC CCG CTC CTT GGC CAC GGC GCA CGA CTG
 <S T D D L L L T Q S R S Y R S V P P G A G P E K G V A C S Q

FIG.12C

3418 GAG CAG CGG GTC CAC CCG GAC CTG CTC CTG AAG CCC AGA GTC CCC CAG TCG TAC GTT GCT CGG CAC GCC CAG GTC GGC CGG GTC CAG CAG
< L L P D V R V Q E Q L G S D G L R V N S P V G L D A P D L L
3508 GGC CTC CTG GCC GAT CTC GGT CCG GCC GGA CCG CTC CCG GTC AGA CGC GCG CCA CCC GTC GAC CCA GGA CAT CCG CGG CGC GAG GTG
< A E Q G I E T R G S R E P E T S A R W G D V W S M P P A L H
3598 CCC GCC GGC CCG GCC GAC CGC CAC GGC GAA GAC CGA GAG TAC GGC CAG CAC GGC CGC GGC CGC CAT CGC CGT ACG CCG GCT GCG
< G G A R G G V A V A F V S L V A L V A A A A M A T R R S R
3688 GCG GCG CCG GGC GCG GAT GTC CGC GCG CTC GGG CCA ACG GAC GTC CCG CAG GTC CCG GTG CAT CCGTTCCGCCAACGTCAAGTG TCA CCG
< R R A R A R I D A P E P W R V D R L D R H M < • A
3782 ATC GGC GGC CTC CTC CAG GTC AGA GAC GGC GAG CAG CCC GGC GAG CGC GGC ACG CCC CCG GGA GAG ACG GGC TTT CAC GGT GCC GAC CCG
< D A A E E L D S V A L L G A L A A R G R S L R A K V T G V P
3872 GGC GGC GGT CTC CCG TGC CAC CTC GGC CAC CCG CAT GCC GAG CAG GTA GTG CAG GGC GAT GGC GGT GCG CTG CGC CTC GGC CAG CCG GCG
< A A T E R A V E A V P M G L L Y H L A I A T R Q A E P L R R
3962 TAG CGC CGC CAC CAC CTC CAG CGT CCG GGT CCG GGC GGC GGT CTC CCG CGC ACC GTG CCG CAG GTA CCG CCG CGC CCG GCT ACG
< L A A V V E L T A T S P A P V S E P A G H R L Y A R A R S R
4052 CAT GCT GCG CCA CCG GCT CAC CGC GAT CCG GCT CCG CAC CGC CAG CCA GCC CTC CGG ATC GTA CCC GCG TAC GGT CGG CCA GCG
< M S R W R S V A I R S A V V R L W G E P D D Y G R V T P W R
4142 CTG CCA TGC GCG CAT GTA CGC CTC CAG GGC GTC CTG CGC GAT TCC GGT GAT CAT GTA CAC GAA ACC CAG CAA TCG TTG
< Q W A R I Y A E Q V A D Q A E A L N G T I M Y V F G L L R Q
4232 CCG GCT GCC CCG GTA GAA CTC GTC GAA CCC CTC GGC GTC CCG CAT CCGCCACCTCCCGTGTCGCAGGGACAGCCCTGGCGGTGTGCCCGTTGCCCGACCGG
< R S G R Y F E D F G E A D P M
4338 CCGGCTTCTCCCTCCCGGGGGTCCC GGCGGGTCTCCCGGGGTCTCCCGGGGGTCTCCCGGGCGGGCGGGCGGGTGTGTCACGTACAGGCCGGCGGGCGGCTTCGG
4459 CAGCGAACAGCACCGTCCGAGAATCGGGTGC CGCGCGGAGTGTCGAGGGCGCGGGTGGCGGTGG TCA GAC CGT GAG CCC GGC GTC GGT GAG GAT CCG GCC GGC
< • V T L G A D T L I P G A
4565 GAG CAG CAG GGC GGC GAG GGC GGC CAG GCA GAC GAC GAA GAC ACC GAC CCA GAA CAG GGG CGG GAA CCG CGT CAA CCG GCG
< L L L A G V A L G A L C V V L F V G V W F L P P T L R A

FIG. 12D

4655 GAG CTG GTC GGC GTC GGA CTC CGG CAT CCG GCC ACG GCT GCG CAG CCG CTG CAA CTC GAT CAC CGG ACG CAC GCC GAA CAG CAG GAA
 < L Q D A D S E P M R G R S R L R Q L E I V P R V G G F L L F
 4745 CCA GAC CGA GGT CCA GGC GAA CGC GGC CTG CAC CTG CGG GGC GGA GTA CCA GGA GAC GGC GAA CAG ACC GCC GGT GGC GAG CAG CGA
 < W V S T W A F A A Q V Q P P A Y W S V A F V L G G T A L L S
 4835 CAG TGC CCC GTA GAC GTT GCG GAT CAT CGC CAG CAT GGC CAG CAG CAG CAC CGT CAC CGA GAG CAG CAT GGT GAT CCG GTT CCC GGC
 < L A G Y V N R I M A L M A L L L V V T V S L L M T I R N G A
 4925 GAG CAG CCA CGC CCC GGC CAG CCC GAG CAG GGT CCG GGC GAC GTA CCC GGC GAA CAG GGT GAG GAT CAT GCC CAG CCC GGT GGC GGC GGC
 < L L W A G A L G L L T P A V Y G A F L T L I M G L G T P R G
 5015 GGC CGA CAG GGT GAG CCC GGA GGT GTC CGA GTG CAG CCG GAT GCC GCG CAG CTT CCG CCC GGT GAG CAG GGC GGC CAG CGC ATG ACC GCC
 < A S L T L G S T D S H L R I G R L K R G T L L A A L A H G G
 5105 CTC GTG GGC GAT GGT CAC CGC GTT ACG CGC GAC CCG CCA GGG CAC CCG GGT GGC GAC CAC CGC CAG CGC GGC GGC GGT GGC CAG GAC
 < E H A I T V A N R A V R W P V R T A V V A L A V A A T A L V
 5195 CAG CAG CGG TGG GTC GGC TTG CGC GGC GAC GAG TTC GTT CCA GAC GAC GCT CAG GCC GTC GAT CAG GTC CAC GGG GCC GCA GCC TAG
 < L L P P P D P Q A G V L E N W V S L G D I L D V P G C G I
 5285 CGG CCC CGG GGT TCG CGC GGC GGC CCG CCA CGG CCG GCG TGC CCG GCC CGG GCC ACC AGC GCC GGC GGC CAC GCCCGCGC
 < P G P G T R A G R A R W P R P A R G P G P R G A G P R V
 5378 TGACCGGACCGG TCA GGT CGC GGC CAC CCC GGT CAG GTC GCC TGC GAC GAA GGC CGC CGC TCT GGT GCC CAC CCG CAA CCG CCG CCG
 < . T A P V G T L D G A V F A A A R T G V R L R R
 5470 AGG GCG GAC CTC ACC GAC CGG CGG CAC CTT GCG TCC ACG TAG GAC CAC GGC GAG CAC CCC GGT CGG CGG CAG CAC GGA AGC GAC CCT GGT
 < P R V E G V P P V K R G R L V V A L V G T P P L V S A V R T
 5560 CAG CAT CCC GGG CAG GCC CTC CCC GGC CCG CTC CCC CTG CCA GCT CGT CTG CTC CCC GTA CCG CAG GTC GGT CAC GAC CAG GTC GGG GGT
 < L M G P L G E G A R E G Q W S T Q E G Y P L D T V V L D P T
 5650 CAT GCC CGC GAC GGC CTC GGT GAG GGC CAC GCG GTC GAA CAC GTC GGC CCG CCG CAG CGG GGC GCC TGC CGC GTC CAG
 < M G A V A E T L A V R D F V D A R R V A Y P L P G G A A D L

FIG.12E

5740 ACG GGC GCG CAG CCG GTG GGC GGC GGC GGC CTC CGC GTA GTG CGG CTT GTC GAA CGC CTC GGC GCG TTG GCG CAG CTC GCG GGC CCG
<R A R L R H A A A A A E A Y H P K D F A E A R Q A L E R A R
5830 CGT GTC GAG CCC GGC GCC GGT CAG CAG GCC GAG GTT GGC CCG AGC AAG GTC GAG GGC CGC CTC GTC GAC GTC GGA GGC GAG CAG CCC GGC
<T D L G A G T L L G L N A R A L D L A A E D V D S A L L G A
5920 AAG GCT CCG CCG GTG CAG CAG CGC GAG CAC CGT CAG CAG GTA GCC GCT GCC GCA CGG GTC CCA GAC GGT GGC CCG GGC GGA CGT CCG
<L S P R H L L A L V T L L Y G S G C C P D W V T A P A S T P
6010 GCG CAA CTC CAG CGC GGT TTG CAG GAC CTC GGA GGC GAG CCG CAC CGG GAA CGC CGG CGC CGA GCG CAA CAC GGC GCC ACT
<R L E L A T Q L V E S A L R V P F A P F G P A S R L V A G S
6100 GGC CAG GTC GGC GTA CCG ACC GCG TAC GGT TTC GTG CCG GTA AGT CAC ATG CCC TCC CCG GCG CAC CCT ACC AAT CCG GCA CCG CCG GGC
<A L D G Y A G R V T E H R Y T V
6190 CCG G TCA GGC AGG CCG GGA CTC GAT CCA GTG GAA GTC GGT GGG AGG CAG CGG CGT GAC GTC CTC CAG GGA CAG CCC CCG CTT GCC GCA CAG
<• A P R S E I W H F D T P P L P T V D E L S L G A K G C L
6281 CCG TTC CAG GTC GCC TCG GGT CCG CTC CAG GCC CTG CCC GTT GAC CAG CAT CCC CAC GTC GGT CAG GTA CCG CAG CCG GTT GGC CCG CCG
<R E L D G R T R E L G Q G N V L M G V D T L Y A L A N A A P
6371 GCC GAC CAC GTC CCG CAG CAC GTG GTC GAT CAT GAC GAT CCG GCC GCC CCG GGC GAC CGC CTC GGC ACA GTG CCG GAG GAT TCC CGT CCG
<G V V D P L V H D I M V I R G G P A V A E A C H R L I G T A
6461 CCG GCC GTC GCC CCA ACC GTG GAT CAC ACT TTT GAG CAG GTA GAG GTC GGC GGC GAC CCT CTC GAA GAA GTC ACC CAC CTC GAT
<R G D G W G H I V S K L L Y L D A D A P V R E F D G V E I
6551 CCG GCA CCG GTC GCC GAC CCC GGC GCG CAG GTT CCC CCG CCG CTC CCG GCT GCC GCT GTC GTA GAG CAC GCC CCG CAC GCC
<R C R D G V G A R R L N G A A E A S G S A S D Y L V G R V G
6641 GGT CCG GGC GAG CAC GGC GGC CAG GGT GCC GTC TCC GCC GCC CAC CAC CGT CCG CAC GCC GGC CAG GTC GGT ACG CTC
<P N A A L V A A L L T G D G G V D V V T R V G A L D T R E
6731 GGC AAC GGC CCG GAC GCT GTG GGT CAC CTG GCT CAT CCG CCG GTT GTA CAG CTC GGA AAG GTC GGG TCG CCC GCC CAC GTA GCT GAA
<A V A A A V S H T V Q S M A A N Y L E S L D P R G G V Y S F

FIG.12F

6821 GAA GTC GGT GCC GAA GAT GCC GTC GAA GGC CGG CTC GCC GGT GCG GAC GCT GTG CGC CAG GCC GTC CCA GGC CGT GGT CAT GGC CGG GTC
 <F D T G F I G D F A P E G T R V S H A L G D W A T T M A P D
 6911 GGT CAG CAT CCG CCC CAG CGG GCG CAG CGT GCC GGG TCG GTC CCC ACG CAG CAG CGC CCC CAT CCG GGC GAG CGC GAA CCG GCC GGG TGT
 <T L M R A L P R L T G P R D G R L L A G M P A L A F R G P T
 7001 GGT CTC GGT GAG CAC CCG CAG CGC GGC CAG CAC CCG GAA CAT GGT GTC CGC TCG GGC GTC GTA CCG CAG CGC CAA CTC CTG
 <T E T L V R L A A L A R L V R F M T D A R A D Y R L A L E Q
 7091 CCG GGT GCG CTC GTC GTC GGC GAT CCG GTC GGC CAG CCC CAG CCG GAC GCA GTA GGC GAC CAG CCG GCT GGC CAT CCC GCC GAA CAC CAA
 <P T R E D D G I A D P L G L R V C Y G V L R S A M G G F V L
 7181 CCG CAT CAG CTC CCG CCA GGC GGC GTC CGC GGT CTC CGC CCG GCG GGC GCT GGT GTC GTC GGT CGT GGC CC GCTGTCGTCGTCGCGGA
 <R M L E P W A A D A G T Q A R R A S P E D T T A R E D T D P V
 7276 CCG TCA TCG GAC CCG GGC GGC CAG GCC GAT CCG CAG CCC GAT GCG CAC GGC CCG TTC GAC CCG CGA GTA GTC GCC GTC CCG GCG GTC CAG
 <T M
 < R V P E A A P L G L G I R V A R E V P S Y D G D P R D L
 7366 GTC CAG CTC GCC CAC CCG CTG CAG GCT CCG CTG GGC CAT GAA CCG GCG CCG GGT GCC CAC CCG GGT GTG CAC CAG GAA CCG
 <D L E G V P Q L S P Q A M F R P R T G T N A V P T H V L F P
 7456 GTG GCA CAG GTA GAC ACC GGC GCG TCC GGT GGC GGA GGC GAG CCG GCG GTC CCG GCC GAC GTC GCC CAC GTC GAG GTA GGT GCC CTC
 <H C L Y V D G A R G T A S A L P R D R G V D G V D L Y T G E
 7546 CCG GCC GTA CCG TTC GAG CAG CCG CCG CAC GTC CAG GTG GGA GCC GAC CCT GAC CAG CGT CCG CGC CTC CCG CTC GTC GGT GTC GGA GAA
 <P G Y P E L L P P V D L H S G V R V L T P A E R E D T D S F
 7636 GAG GAA CAG CAG CAG GGC CCG CCC CCG CGA CCG GAG GTT GCA GCG GAA GAC CTC CCG GTA GTT GGG CCG GAC CAG GTC CAG CTC GCC
 <L F L L L A R G R S R L N C R F V E A Y N P P V L D L E G
 7726 CTC CCA GTT CTG GGG GCC CAG CCG CTG CCG GTC GGC CAG GAA ACT GGC GTC GAT GTG CCA GCC GTA GTC CTC GGT CTC CCG GCG
 <E W N Q P G L R Q A D D A L F S A D I H W G Y D E T Q E P R
 7816 CTT GGG CAC CCG GAA CCG GAC CCG GAT CCG GTC CAA CCG CTT CCA GCG CCC CAC CCC GAC GAG CTG GTC GAA GGC GGC GTG
 <K P V P F R V P F T G I R D L P K W R G V G V L Q D F A A H

FIG.12G

7906 CAG CCG GGG CGT GGT GGC GCT GCG CAC GAA GGG CTC GGC GTC CTG GAG GCC CAG CCG GAC CAC CTC GCG GGA CCA GGT GCT CCG GTC CTC
 < L R P T T A S R V F P E A D Q L G L R V V E R S W T S R D E
 7996 GGG GTC CAT GCC GAG TTG CCG CCA CAG CAG TTC GCG ACC CTG CTG CCG GAG CTC GGC CCG GAA CCG CCG CTC CAA CTT CAC GAA CCC GTC
 < P D M G L Q R W L L E R G Q Q A L E A P F A A E L K V F G D
 8086 GGA GAC GAA CCG CTC GAC CTG CTC GCT GCT GAG GAC CTG GGC GCT CAT CCG ACT CCT TCC CCG CCG TTC CCG CCG AGG CCG AGC GAG AGG
 < S V F R E V Q E D S L V Q A S M
 8176 GTC GCA CCC GCG CTG ACC GGA CCG GGC GAC GCG CCT CGT CAA GAT TCG CCA GGT TGA ATG GTA GAC AAG CCG CCA CCG TCA GGG ACT AAC
 < • P S V
 8266 GTT TTC CTC AGC ATC GTC CCG GGC ACC GCG AGA GCG CCG CAC CCC CCG CTC CAC CAC CCG CAA CCA TCG GCT CTC CCC GGG TGC GGC GAT
 < N E E A D D P G G R S R R V G R E V V R L W R S E G P A A I
 8356 GGC GTC GAG CCG GGC CTC CTC CCG CAG CCG GTC GGC CCG CAG CCG CCG GGC CTG GTC CAG CGT GCG GGG GCC GAC
 < G D L R A R A E E P L P R D A A A L A R A Q D L T R P G V
 8446 GAC CGT GGT CAC CCC CCG CCG GTC GTA GAC CCA GGC GTG CCG CAG GTC CCG CAG GGA CAG GCC CAG CTC GAC GGC CAC CTT CCG CAA
 < V T S T V G P A D Y V W A H A L D P L S L G L E V A V K A L
 8536 CCG GCC CAG GGT CCG CCA CAC CCG CTG CCA GTG CCG GCC CGA TGG GGC GTA CCA GGC GGT GAA CCG GGC GTC GCG GGG CTC GCC GTC
 < R G L T R W V P Q W H P G S P A Y W A T F R A D R P E G D
 8626 GGC GAA CCG GTC GGA GAG CAG ACC CAT CCG CAG CCG GCT GTA GGT GAA CAG GCC GAG GCC GTA CTC CCG GCA CAG CCG CAG CAC GTC CCG
 < A F R D S L L G M A L P S Y T F L G L G Y E A C L P L V D R
 8716 CTC GAT CTC GCG TTC CAG CAG GTT GTA CCG CGA CTG CTC GGC CAC CAC CCG GGC GCC CCG GGA CTG CCG CGT GCG CAG CAG GTC GAC
 < E I E R E L L N Y P S Q E A V V P A A G R S Q A T R L L D V
 8806 GAT CCG CCA GCT GGG CAC CGT GCC CAG CCG GGG CTG GTC GGC CAG CTC GTA TGC CGT GGC CAC GGT GGA GGT GCC CAC GTA GCG GAC CTT
 < I R W S P V T G L R P Q D A L E Y A T P V T S T G V Y R V K
 8896 GCC CGA GCG GAC CAG GTC GTC GAG GGC GGA CAC CGT CTC CTC CCG AGT GTC CCG GTG ACG GTG CAG GTA GAG CAG GTC GAT GTG
 < G S R V L D D L A S V T E E V P T D P D H R H L Y L L D I H

FIG.12H

10190 CTC GCC TTC GTC GCC ACC AGG GCC CGC CAC CTG TAC GTC AAC AAC CCC GTC GGG AAG TAC CTC GAC AAG ACC CTG GAC GGG CAC TTC CAG
 > L A F V A T R A R A H L Y V N N P V G K Y L D K S L D G H F Q
 10280 GGC GAG GCC GTG GTC AAC CTT GCG CTG AGC ACC GGC CTG CTG CGC GAC GTC ATC GAC AAC CAG GAC GGC GTG CGG CGG CAG TCC
 > G E A V V N L A L S T G L L R D V I D I H D N Q A V R R Q S
 10370 CCG GCG TTC CTC GAC GCG TAC CCG CCG GCG CCG GGC TGG GGC TGC GTG GCG GAG AGC CGG AGC ATC CCG TGG ACC TAC TAC TGG CAG GCG
 > R A F L D A Y R P G P G W A C V A E S R T I P W S Y Y W Q A
 10460 CTC TAC CCG GCC GGC GAG GCG GCC CCG GCA CCC GGG CCG GAT TGA GGTGACCGGCCGAGCGGGCGACCGCGCGTCTCGCGGCGCTCC
 > L Y R A V E A A P A P G R D .
 10566 GGCCTGTCGCACCECT GTG CTG GCC GCG CTC GCC GAC CCG GCG GTC ACC GTC CCG GCC GTC GCC CGC CGG GCT GCC GTG CTG CCC GCC GCG
 > V L A A L A D R A V T V R A V A R A A V L P A A
 10659 CCG GGC CGC GCG TTT GAG GTG GTA CCG GGC GAC CTG ACC GAC CCG GGA GCC CTG GCG GCG GTA CCG GAC GCG ACG GCC GTG GTC
 > P G R A A F E V V R A D L T D R G A L A A A V R D A T A V V
 10749 AAC CTC ACC CTG GAC AGT TCC GGC TGG CCG GGC GGC GAC GAC CCG AGC GCG GTC AAC GTC GAG CTG ACC CCG GAA CTC GTC GCG
 > N L T L D S S G W R G A D D R S A R V N V E L T R E L V G
 10839 ATG CTC CGC CCC GCG GCG GGC ACG ACC ACA CTG GTC TTC GCC GGC TCC GCC CAG GTG GGC CCG CCC CCG ATC CCG ATC
 > M L R P G P G G T P T T L V F A G S A S Q V G R P R I P I
 10929 GAC GGC ACC GAG CCG GAC CAC CCC GGC TAC GAC CCG CAG AAG CAG GCC GCG GAG TCG CTG GTC GTG GCG GCC ACC GCG GCG GCG
 > D G T E P D H P A T P Y D R Q K Q A A E S L V V A A T G A G
 11019 GTC GTG AAC GGG GTG TCG CTG CGA CTG CCC ACC GTG TTC GGC CCG GTG CCG GGC GGC CCC GAC CCG GGC GTG TCC ACG ATG
 > V V N G V S L R L P T V F G P P G A G P D R G V V S T M
 11109 ATC CGC CCG GCG CTG TCC GGA CCG CCA CTG ACC ATG TGG CAC GAC GGC CCG GTG CAA CCG CAA CTG CTG TAC GTG GCC GAC GCC GCG GCG
 > I R R A L S G A P L T M W H D G R V Q R Q L L Y V A D A A A
 11199 GCC TTC GTG GCG GCG CTG GAC CAC CCC GGG CCG CTG ACC GGC CCG CAC TGG CCG CTC GGC GAC GCG GGT GAA CCG CTC GCG GAC CTG
 > A F V A A L D H P G A L T G R H W P L G D G R G E R L G D L

FIG.12J


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11289 TTC CGC GCC ATC GCC GCC CTG GTG GCC GAG CGG ACC GGT CGG CCA CCG GTG CCG GTG GCC CTG CCC CCG GCC GAG GCC CGG GTC
    > F R A I A A L V A E R T G R P P V L A V P P P D E A R V
11379 AGC GAC TTC CAC GAC ATG GTC GTT GAC GCC TCG GCC TTC CAG GCG GTC ACC GGG TGG GCG CCC CCG GTG CCG TTG CCG CTC GCG CTG GAC
    > S D F H D M V V D A S A F Q A V T G W A P R V P L R L A L D
11469 CGC ACC GTC GCG GCG CTC GCC CGC GAC GAC AGC GGC CCC GAG GCC CCG GGC GGC GTC GGC CCG ACG CGG GCG GAT CAG GCC CGG
    > R T V A A L A R D D S G P E A P G G V G P T R A D Q A R
11553 AAG CCG GAC TCG ATC TCC AGG CAG GTC CCG TAG TCGGGCAGCAACCCACGGGCGAGCGCCTGGTGGAAAGGTGATCGCGGTGCGGTCCTCCGCTCCGACAGGATCGGTTGAC
    > K P D S I S R Q V R .
11663 GTCCTCGGGGATGGGCAGGCCAGGCCAGCCCGGGGTGAGCGCGTTCGAGCGCCAGTTGTTCTCGAAGACGTACTCCTGGGACAGGACGTACGACATGACGGTGTGTCGGCCAGGGCGACGAAC
11784 ATGTGCGCGACCCCGACCCGGCAGGTAGACCGCCTGGAACTCCTGCTGTGAGCACCACGCTGTCCACTTGCCGAACTGCGGTGAGCCACCACCCGACGTCGAGGACAGGTGAGCACCC
11905 GGCCGTGCGGGCAGGAGACGAACCTTCGCGGTGCGGGGCGGGGTACGGGTGAAGTGACGCCGCCGAGCGTCCCGGGGGGAGACGCTGTAGCTGGTCTGCCGACAGGGGAACAGCGGGTA
12026 CCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCCGAGAGGAACACCCCGGTAGTCGGGTAGACGGTGGGCGCGAAGGCGTACGGCCCTTCGACGGTCAGCGGGGCGGGCGGACACC
12147 GGCGGG

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FIG.12K